

REPLACEMENT
SHEET

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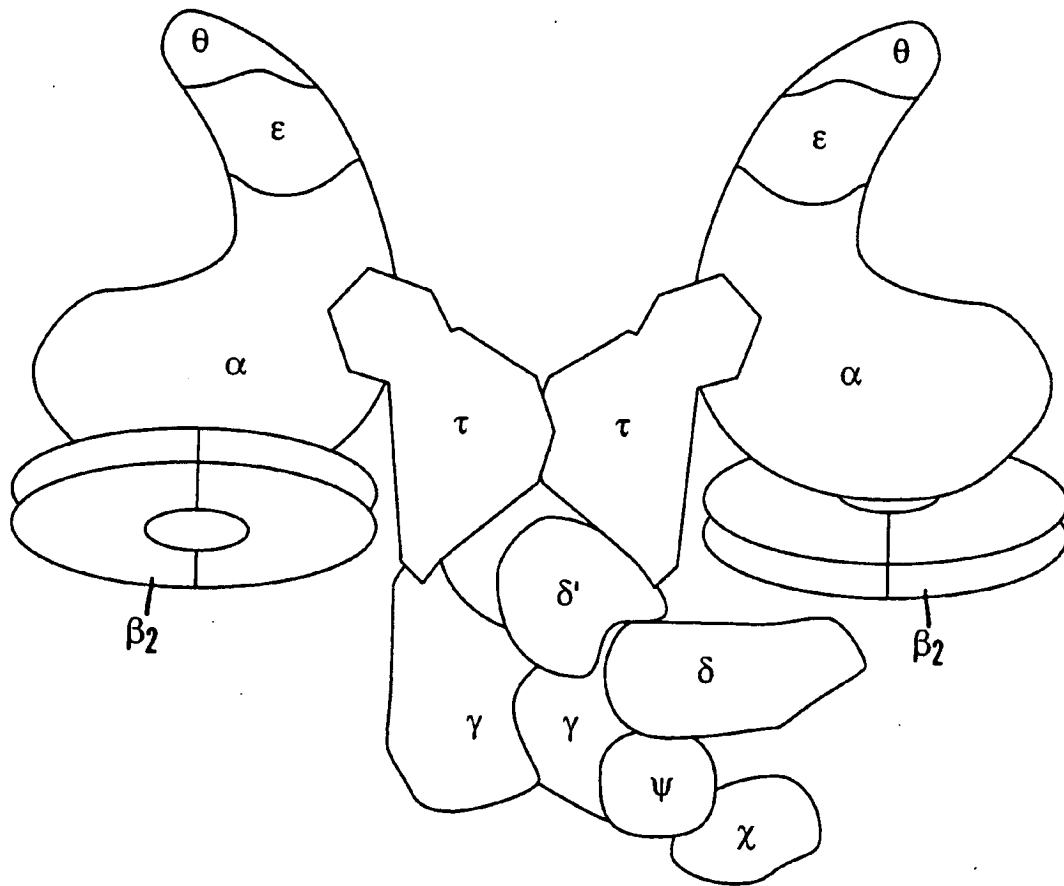


FIG. 1

REPLACEMENT SHEET

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ATP binding

| | |
|-------------|---|
| E. coli | MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHH AYLFSG TRGVGKTSIARLLAK |
| B. subtilis | MSYQALYRVFRPQRFEDVVGQEHITKTLQNALLQKKF SHAYLFSG PRGTGKTSAAKIFAK |
| | *** |
| E. coli | GLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRF |
| B. subtilis | AVNCEHAPVDEPCNECAACKGITNGSISDVIEIDAASNNGVDEIRDIDKVKFAPSAVTY |
| | *** |
| E. coli | KVYLIDEVHMLSRHSFNALL KTLEPP EHVKFLLATDPQKLPVTILSRCLQFHLKALDV |
| B. subtilis | KVYIIDEVHMLSIGAFNALL KTLEPP EHCIFILATTEPHKIPLTIIISRCQRFDFKRITS |
| | *** |

FIG. 2

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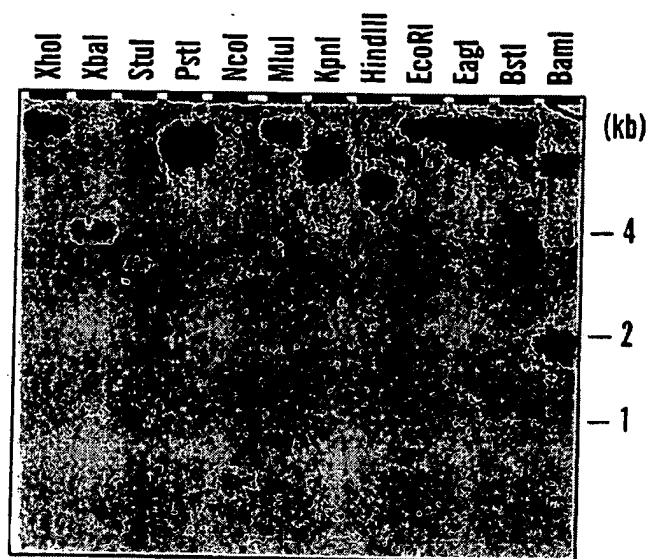


FIG. 3

REPLACEMENT SHEET

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| | | | | | | |
|---|---|---|------------|------------|-------------------|--------------|
| TCCGGGGGTG | GGGTTCCAG | GTAGACCCCG | GCCCCTCCCG | TGAGCCCCTT | TACCCAGGCC | 60 |
| GCCACCTCCT | CCAGGGGGG | CAAGGCGTGC | AAGGAGAGGA | ACGTCCGCAC | <u>CACGCCCTAT</u> | 120 |
| ACTAGCCTT | GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG | met ser ala leu tyr arg phe arg pro leu thr phe gln glu val val | | | <u>S.D.</u> | 180 (17) |
| GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG | gly gln glu his val lys glu pro leu leu leu lys ala ile arg glu gly arg leu ala gln | | | | CAC | 240 (37) |
| GCS TAC CTS TTC TCC GGS AC | | | | | | |
| GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACC GCG AGG CTC CTC GCC | ala tyr leu phe ser gly pro arg gly val val gly lys thr thr thr ala arg leu leu ala | | | | | 300 (57) |
| ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTG TGC CCC CAC TGC CAG GCG | met ala val gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala | | | | | 360 (77) |
| GtG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC AGC AAC AAC TCC GTG | val gln arg gly ala his pro asp val val asp ile asp ala ala ser asn ser val | | | | | 420 (97) |
| GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG | glu asp val arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys | | | | | 480 (117) |
| GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG | val phe ile leu asp Glu ala his met leu ser lys ser ala phe asn ala leu leu lys | | | | ^C | 540 (137) |

FIG. 4A-1

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FIG. 4A-2

REPLACEMENT SHEET

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| | |
|---|---------------|
| GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA | 1140 (337) |
| glu arg leu ala arg arg ser asp ala leu ser leu glu val ala gly | |
| AGG GCC CTG GCC GAG GCC CTA CCC CAG CCC ACC GGC GCT CCT TCC CCA GAG GTC GGC | 1200 (357) |
| arg ala leu ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly | |
| CCC AAG CCG GAA AGC CCC ACC CCG GAA CCC CCA AGG CCC GAG GCG CCC GAC CTG | 1260 (377) |
| pro lys pro glu ser pro pro thr pro pro arg pro glu ala pro asp leu | |
| CGG GAG CGG TGG CGG GCC TTC CTC GAG GCC GGC GGC ACC CTA CGG GCC TTC GTG CGG | 1320 (397) |
| arg glu arg trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg | |
| GAG GCC CGC CGG GAG GTC CGG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC | 1380 (417) |
| glu ala arg pro glu val arg arg glu gly gln leu cys leu ala phe pro glu asp lys ala | |
| TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTC GCC CAG GCC CAT | 1440 (437) |
| phe his tyr arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his | |
| frameshift site | |
| TTC GGG GTG GAG GAG GTC GTC CTC GTC CTC GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG | 1500 (457) |
| phe gly val glu glu val val val val glu glu lys lys ser leu ser pro arg | |

FIG. 4B-1

REPLACEMENT SHEET

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| | |
|---|---------------|
| CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA | 1560 (477) |
| pro arg pro ala pro pro pro pro ala pro pro pro gly pro pro glu glu val | |
| GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GAG GTC CGC CTC | 1620 (497) |
| glu ala glu glu ala ala glu glu pro pro glu ala leu arg val arg leu | |
| CTG GGG GGG CCG GTG CTC TGG GTG CCG CCG CCG CCG GAG GCG CCG GAG GAG GAA | 1680 (517) |
| leu gly gly arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu | |
| CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA | 1740 (529) |
| pro leu ser gln asp glu ile gly thr gly ile * | |
| CGACCTCGGA CAAGAGACCG TGGACAACAT CCTCAAGCGC CTCCGCCGTA | 1820 |
| GGTGGGGGG CTCCAGAAGA TGGTGGCCGA GGGCCGCCCC TGCACGAGG | 1880 |
| GATGACCGCC ACCAAGAAG CCATGGAGGC GGCGGCCACC CTGATCCTCC | 1940 |
| GAACGTCTGC GCCGCCGAGG TCTCCGAGGG CAAGGTGAAC CCCAAGAAGC | 2000 |
| CGCCACCATG CTGAAGAACT TCATCTA | 2027 |

FIG. 4B-2

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[illegible]

FIG. 4C

REPLACEMENT SHEET

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| | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | ser | ala | leu | tyr | arg | arg | phe | arg | pro | leu | thr | phe | gln | glu | val | val | gln | glu | gln | glu | 20 |
| his | val | lys | glu | pro | arg | leu | lys | ala | ile | arg | glu | gly | arg | leu | ala | ala | tyr | leu | leu | 40 | |
| phe | ser | gly | pro | arg | gly | val | gly | lys | thr | thr | thr | ala | ala | leu | ala | met | ala | val | ala | 60 | |
| gly | cys | gln | gly | pro | asp | pro | pro | cys | gly | val | cys | pro | his | cys | gln | ala | val | gln | arg | 80 | |
| gly | ala | his | pro | arg | val | val | asp | ile | asp | ala | ala | ser | asn | asn | ser | val | glu | asp | val | 100 | |
| arg | glu | leu | arg | glu | arg | ile | his | leu | ala | pro | leu | ser | ala | pro | arg | lys | phe | ile | ile | 120 | |
| leu | asp | glu | ala | his | met | leu | ser | lys | ser | ala | phe | asn | ala | leu | leu | lys | thr | leu | glu | 140 | |
| glu | pro | pro | pro | his | val | leu | phe | leu | phe | ala | thr | thr | arg | leu | glu | arg | met | pro | pro | 160 | |
| thr | ile | leu | ser | arg | thr | thr | gln | his | thr | arg | arg | arg | glu | leu | thr | glu | glu | ile | ala | 180 | |
| phe | lys | leu | arg | arg | ile | leu | glu | ala | val | gly | arg | glu | ala | glu | glu | glu | ala | leu | leu | 200 | |
| leu | leu | ala | arg | leu | ala | ala | asp | gly | ala | leu | arg | asp | ala | glu | ser | leu | glu | arg | phe | 220 | |
| leu | thr | gly | val | gly | pro | leu | thr | arg | lys | glu | val | glu | arg | ala | leu | gly | ser | pro | pro | 240 | |
| gly | leu | ala | arg | arg | glu | leu | thr | gly | glu | tyr | ala | ala | pro | arg | ser | leu | ala | glu | leu | 260 | |
| leu | glu | val | arg | phe | ala | arg | leu | gly | ala | met | phe | ala | gly | leu | ala | thr | pro | gly | leu | 280 | |
| ala | pro | pro | gln | ala | ala | leu | ile | ala | ala | thr | ala | ala | pro | ala | ala | gly | thr | leu | pro | 300 | |
| ala | arg | arg | ser | asp | ala | leu | ser | leu | glu | val | ala | leu | leu | asp | glu | ala | met | glu | arg | 320 | |
| ala | ala | glu | ala | leu | pro | gln | pro | gln | thr | gly | ala | pro | ser | glu | glu | ala | gly | arg | ala | 340 | |
| glu | ser | pro | pro | thr | pro | glu | pro | glu | arg | pro | glu | glu | pro | glu | val | gly | pro | lys | pro | 360 | |
| trp | arg | ala | phe | leu | glu | ala | leu | ala | pro | thr | leu | arg | ala | phe | asp | leu | arg | glu | arg | 380 | |
| pro | glu | val | arg | glu | gly | gln | lys | val | ala | ala | phe | pro | glu | asp | lys | arg | glu | ala | arg | 400 | |
| arg | lys | ala | ser | glu | gln | lys | val | leu | leu | leu | pro | leu | ala | gln | ala | his | phe | his | tyr | 420 | |
| glu | glu | val | val | leu | val | leu | glu | glu | lys | lys | pro | ser | leu | ala | his | phe | gly | val | val | 440 | |
| ala | pro | pro | pro | glu | ala | pro | ala | pro | pro | gly | pro | pro | leu | glu | val | arg | pro | arg | pro | 460 | |
| glu | ala | ala | glu | glu | ala | pro | glu | glu | ala | ala | pro | pro | glu | glu | val | glu | ala | ala | glu | 480 | |
| arg | val | leu | trp | val | arg | arg | pro | arg | thr | ala | arg | arg | val | val | arg | leu | leu | gly | gly | 500 | |
| gln | asp | glu | ile | gly | gly | thr | gly | thr | arg | arg | glu | ala | pro | glu | glu | pro | leu | ser | ser | 520 | |
| | | | | | | | | | | | | | | | | | | | | 529 | |

FIG. 4D

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FIG. 4E

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FIG. 4F

REPLACEMENT SHEET

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| | | | |
|----------|--|----------|-----|
| E. coli | MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAK | ATP site | 60 |
| H. inf. |K.....II.....KDN.L.....F..... | | 60 |
| B. sub. |A.Y.VF...R.E.....ITKT.Q.A.LQKKFS.....P.T....A.KIF.. | | 60 |
| C. cres. | DA.T....Y.R..E.LI...AMVRT...AF.T...A.FMLT.V.....TT....R | | 113 |
| M. gen. | -MH..FYQ.Y..IN.KQTL...SIRKI.V.AINRDKLPNG.I...E.T...TF.KII.. | | 59 |
| T. th. | --VSA.Y.RF..L..QE.....KEP.LKAIRE..LAQ.....P.....TT.....M | | 58 |
| | Zn ⁺⁺ finger | | |
| | * * * | | |
| E. coli | GLNCET---- | | 116 |
| H. inf. |VH-----V.....E.E..KA....N.I.....E.....K.V | | 116 |
| B. sub. | AV...H-----APVDE..NE.AA.KG.TN.SIS.V.....NNG.DEI..IR.K.KF..S | | 116 |
| C. cres. | A..Y..DTVK.PSVDLTTEGYH..S.IE..HM.VL.L.....DEM.E...G.R...V | | 173 |
| M. gen. | AI..LN-----WDQIDV.NS..V.KS.NTNSAI.IV.....KNGIN.I.E.VE..FNH.F | | 115 |
| T. th. | AVG.QG-----EDP.....PH.QAVQR.AHP.VVD.....NNS...V.E.ERIH..L | | 112 |
| E. coli | RGRFKVYLIDEVHMLSRHSFNALLKTLLEPPPEHVKFLLATDPQKLPVTILSRCLQFHLK | | 176 |
| H. inf. | V.....I.....IGA.....CI.I.....E.H.I.L.I...QR.DF. | | 176 |
| B. sub. | EA.Y...I.....TAA.....P.A..IF...EIR.V.....QR.D.R | | 233 |
| C. cres. | TFKK...IL..A...TTQ.WGG.....S.PY.L.IFT..EFN.I.L.....QS.FF. | | 175 |
| M. gen. | SAPR..FIL..A...KSA.....P..L.VF...E.ERM.P.....TQH.RFR | | 172 |
| T. th. | | | |

FIG. 5A

REPLACEMENT SHEET

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| | | |
|----------|---|-----|
| E. coli | ALDVEQIRHQLEHILNEEHIAHEPRALQLLARAAEGSLRDALSLTDQAIASGDGQ--VST | 234 |
| H. inf. | ...ET..SQH.A...TQ.N.PF.DP..VK..K.Q..I..S.....M..R.--.TN | 234 |
| B. sub. | RITSQA.VGRMNK.VDA.QLOV.EGS.EII.S..H.GM.....L.....SFSGDI--LKV | 234 |
| C. cres. | RVEPDVLVKHFDR.SAK.GARI.MD..A.I.....V..G...L.....VQTERGQT.TS | 293 |
| M. gen. | KITSDL.LER.ND.AKK.K.KI.KD..IKI.DLSQ.....G...L..LAI.LIVKKL.LL | 235 |
| T. th. | R.TE.E.AFK.RR..EAVGREAA.EE..L....L.D.A....E..LERFLLLEGP---LTR | 229 |
| E. coli | QAVSAMLGTLDDDDQALSLVEAMVEANGERVMAINEAAARGIEWEALLVEMGLLHRIAM | 294 |
| H. inf. | NV..N...L...NYSVDILY.LHQG...LL.RTLQRV.DAAGD.DK..G.CAEK...Q..L | 294 |
| B. sub. | EDALLIT.AVSQLYIGK.AKSLHDK.VSDALETL..LLQQ.KDPKAK.IED.IFYFRDMLL | 294 |
| C. cres. | TV.RD...LA.RS.TIA.Y.HVMAGKTKDALEGFRALWGF.ADPVVMLDV.DHC.AS.V | 353 |
| M. gen. | MLKKHLISLIEMQNL.L.KQFYQ.I | 260 |
| T. th. | KE.ERA..SPPGTGVAEIAASLARGKTAEALG.ARRLYGE.YAPRS.VSGL.EVFRGLY | 289 |

FIG. 5B

REPLACEMENT SHEET

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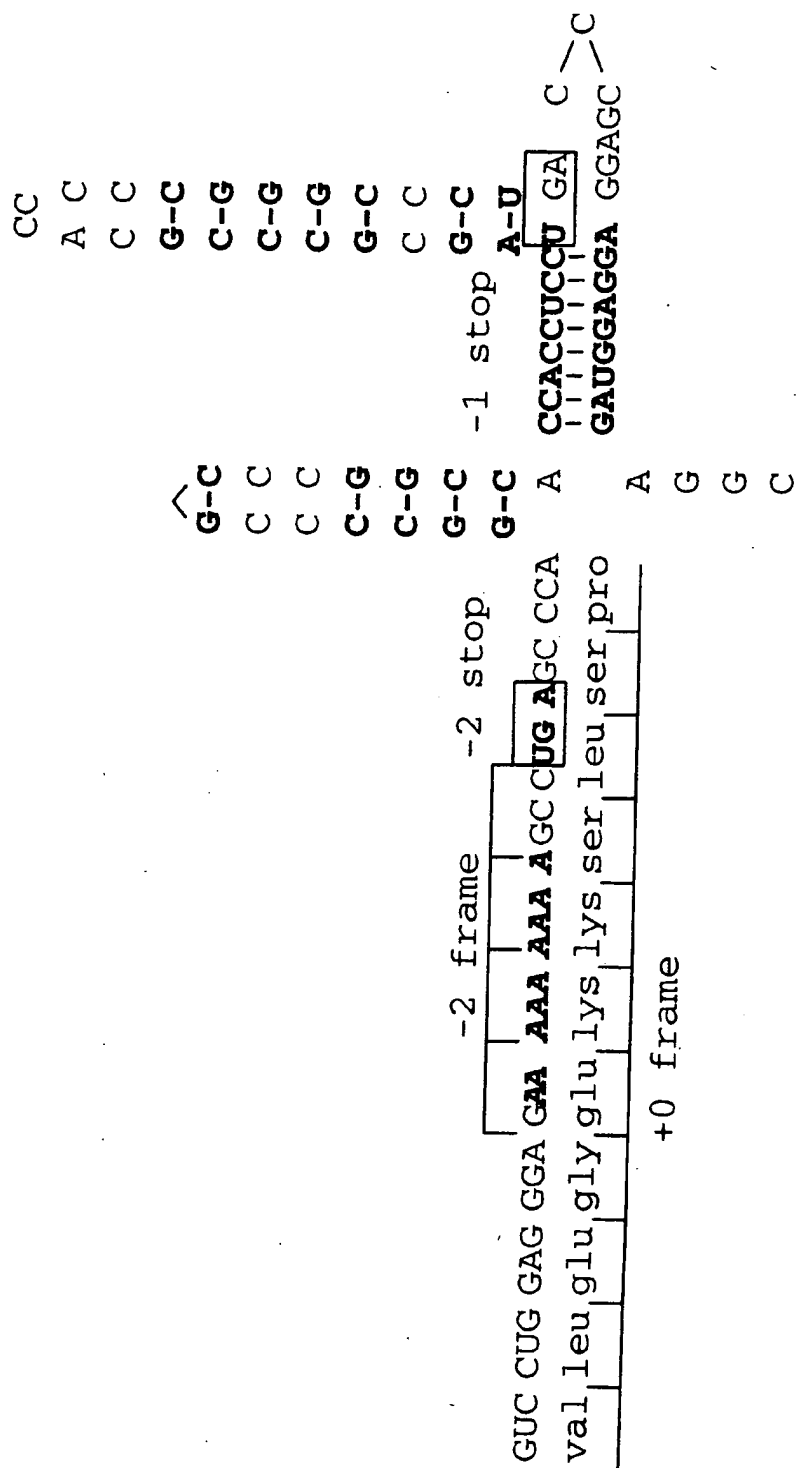


FIG. 6

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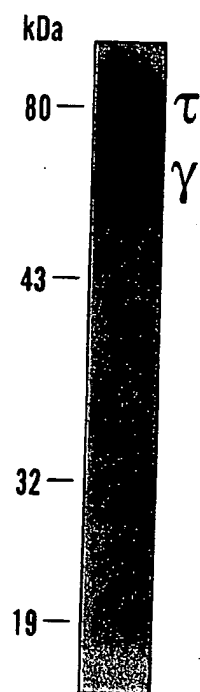


FIG. 7

REPLACEMENT SHEET

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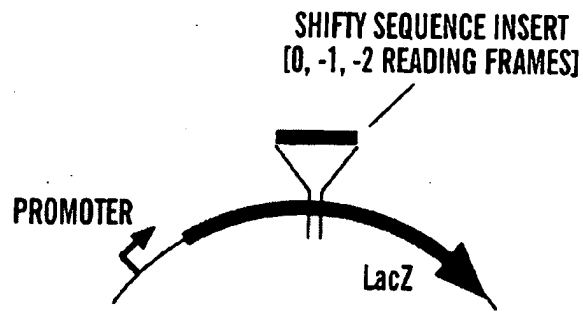


FIG. 8A

| | READING FRAME | BLUE | WHITE |
|-----------------|------------------|------|-------|
| SHIFTY SEQUENCE | 0 | + | |
| | -1 | + | |
| | -2 | + | |
| MUTANT SEQUENCE | 0 | ++ | |
| | -1 | | + |
| | -2 | | + |

FIG. 8B

REPLACEMENT SHEET

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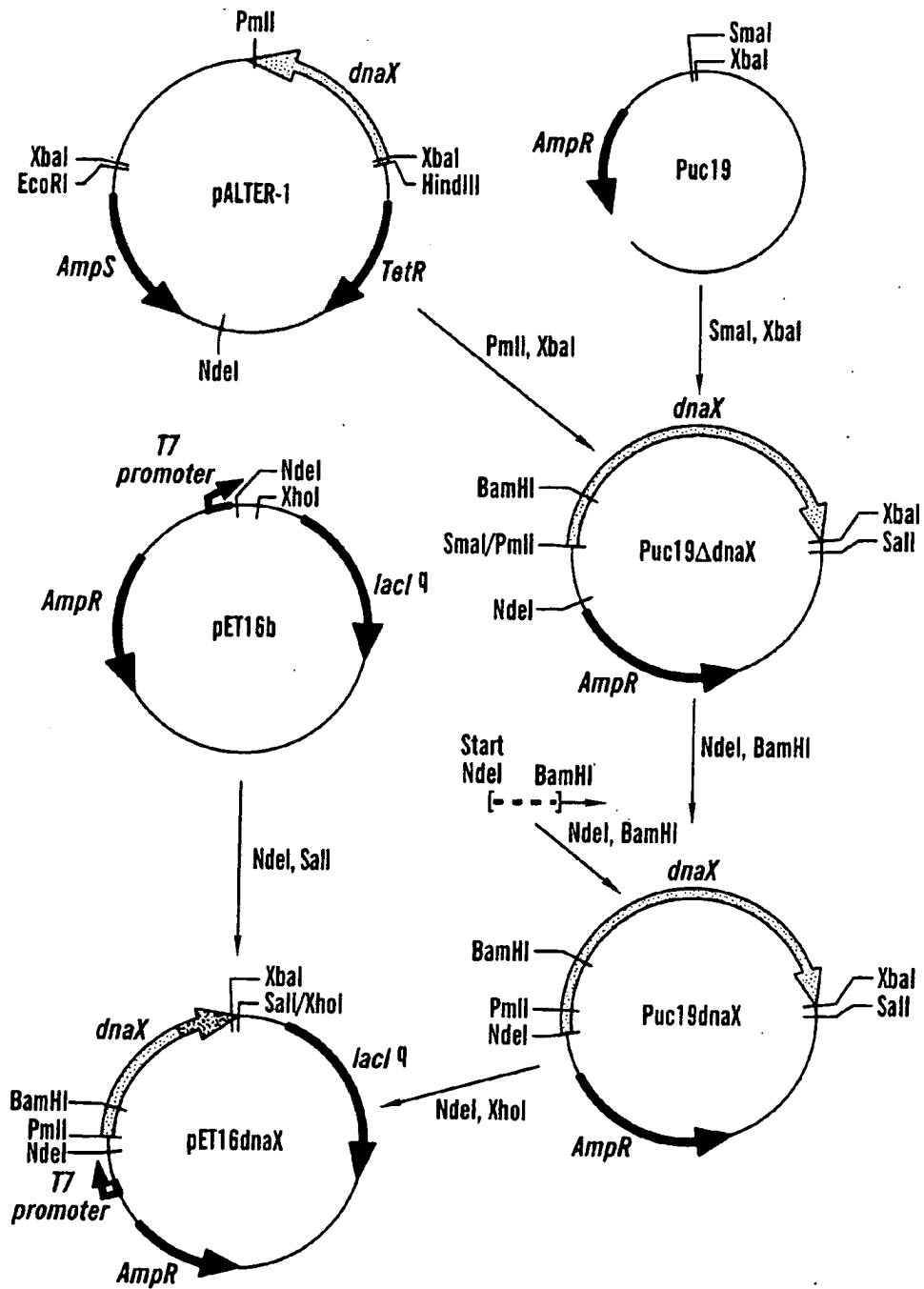


FIG. 9

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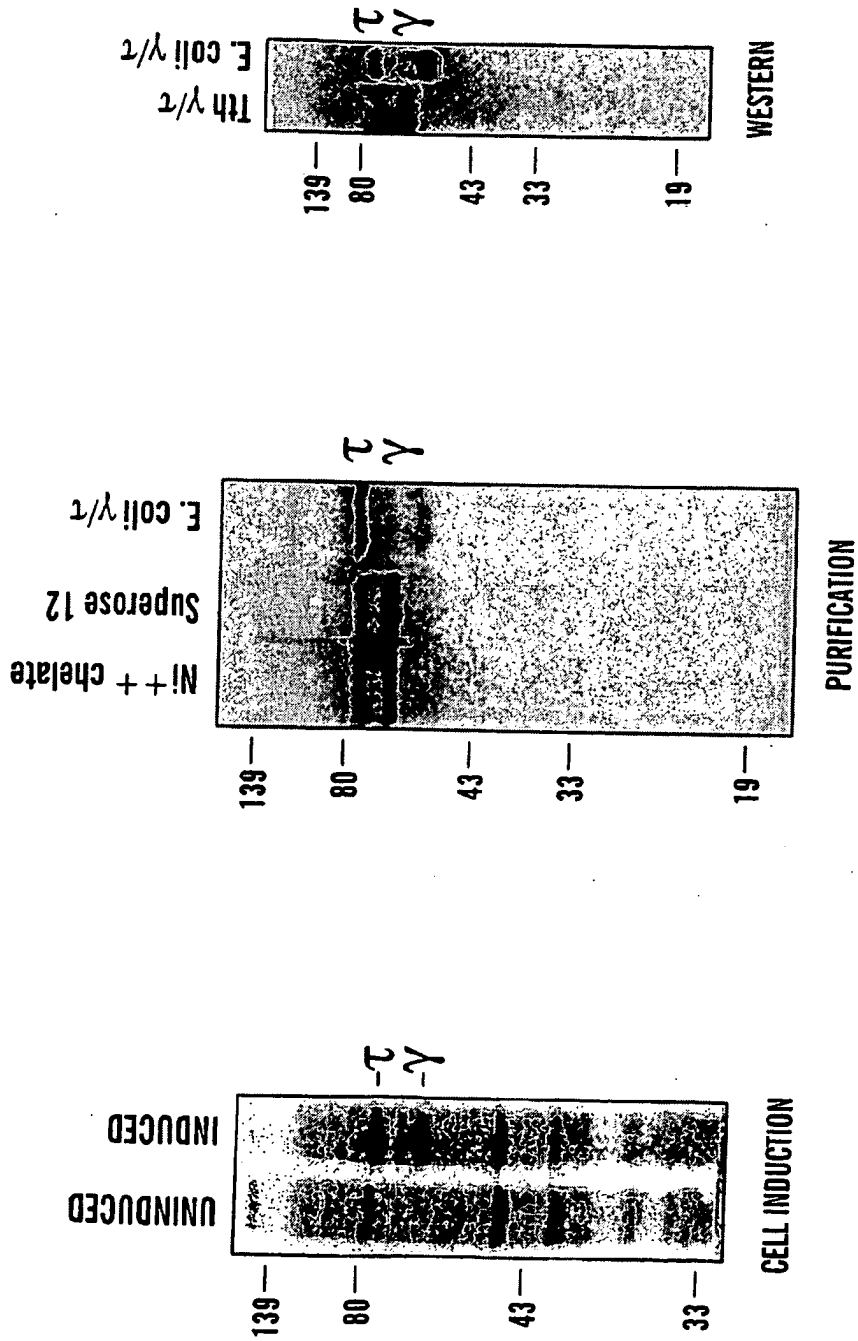


FIG. 10A

FIG. 10B

FIG. 10C

REPLACEMENT
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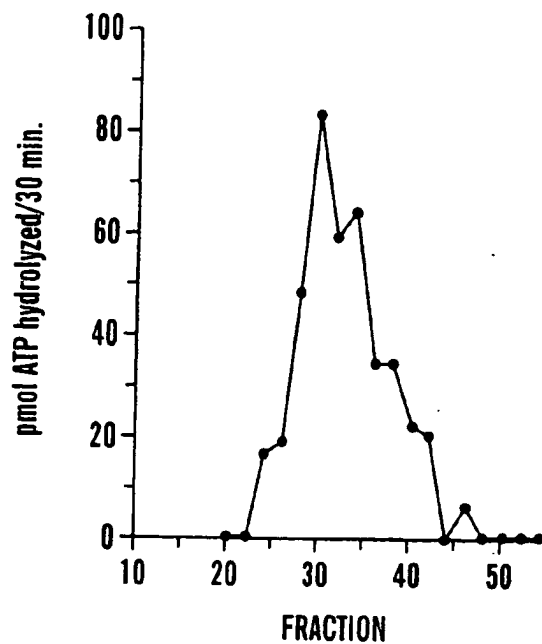


FIG. 11A

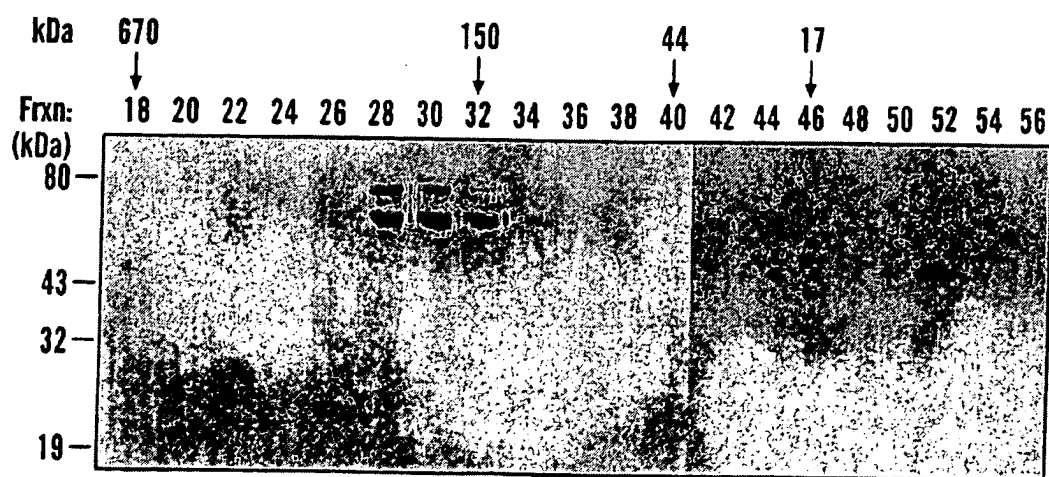


FIG. 11B

REPLACEMENT
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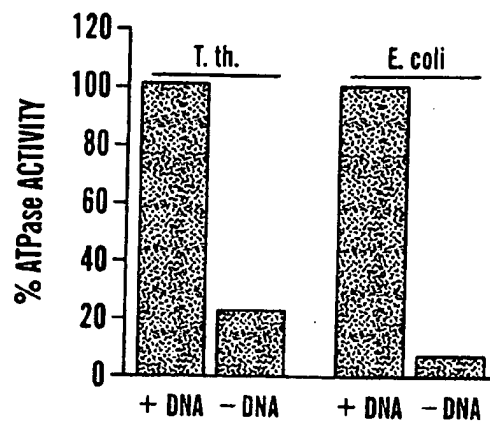


FIG. 12A

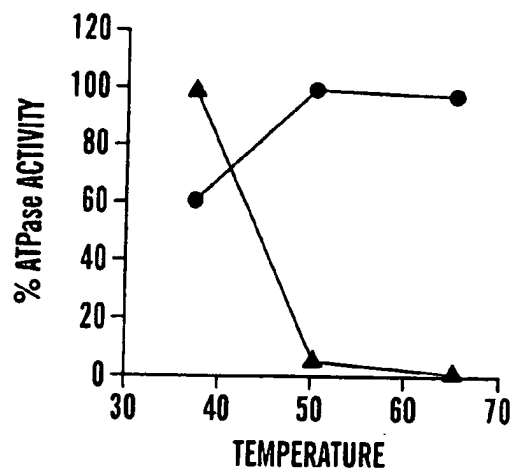


FIG. 12B

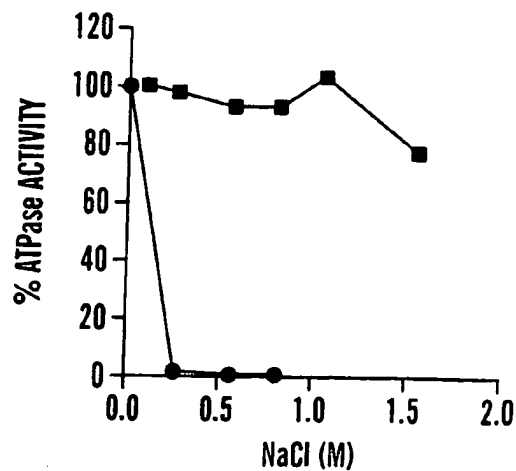


FIG. 12C

REPLACEMENT
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FIG. 13A

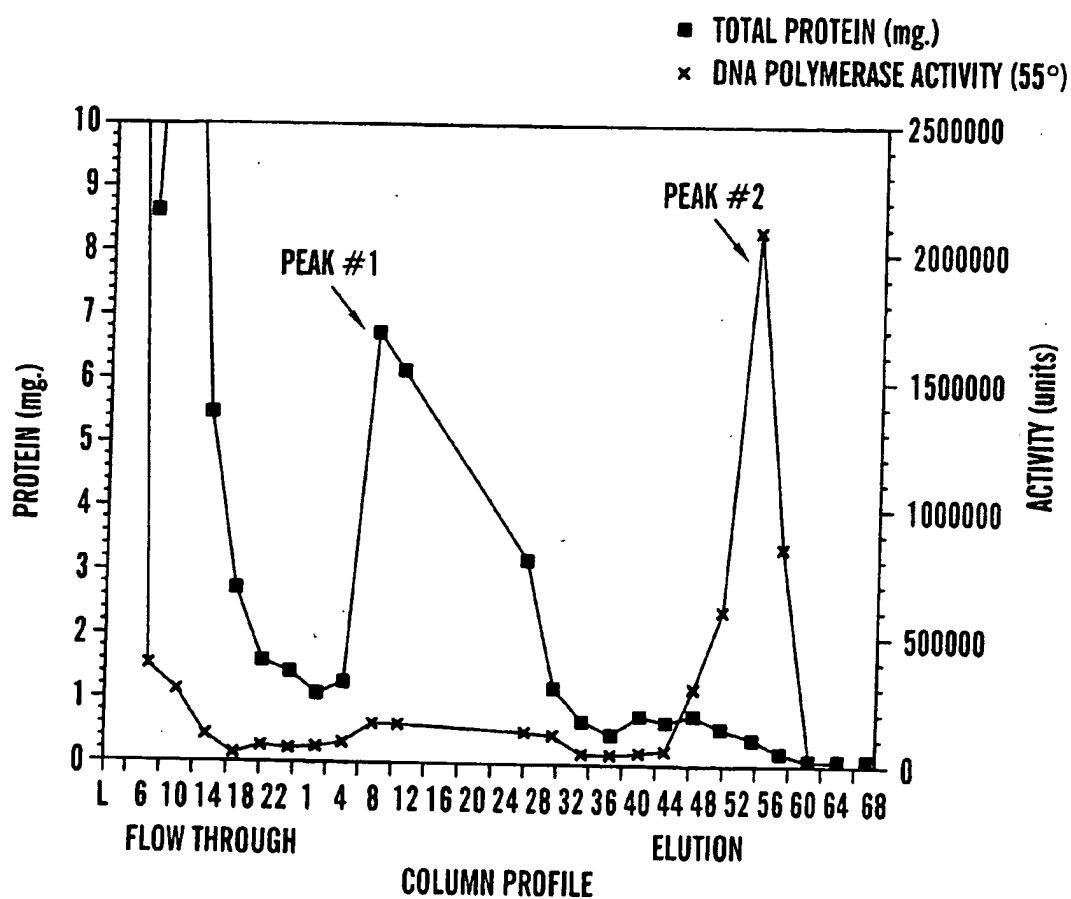


FIG. 13B

ATP AGAROSE STEP COLUMN

REPLACEMENT SHEET

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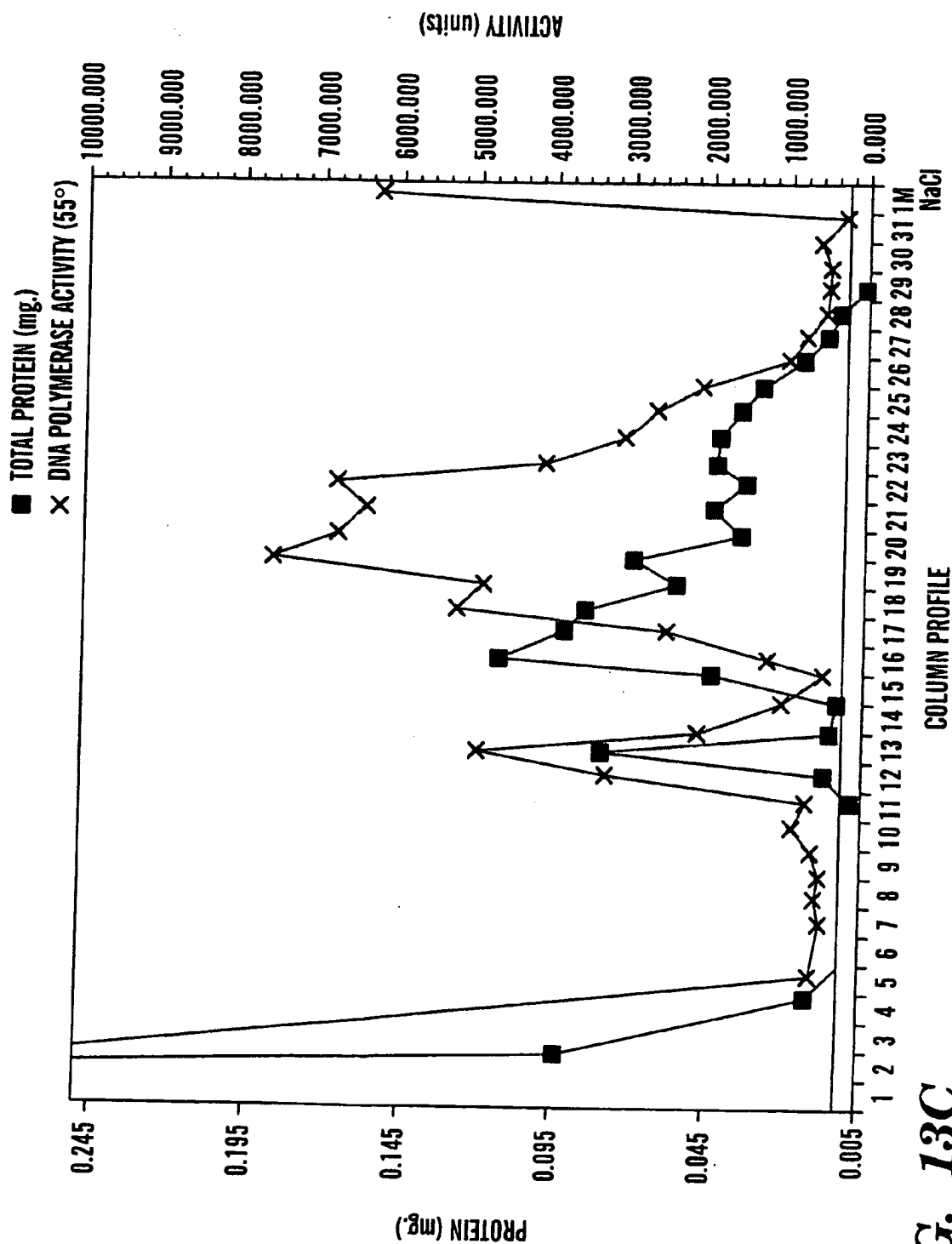


FIG. 13C

REPLACEMENT SHEET

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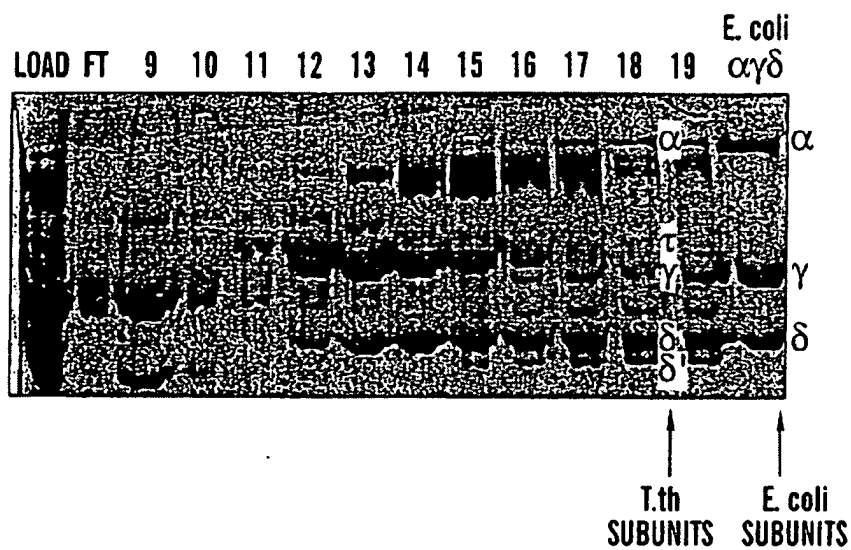


FIG. 14A

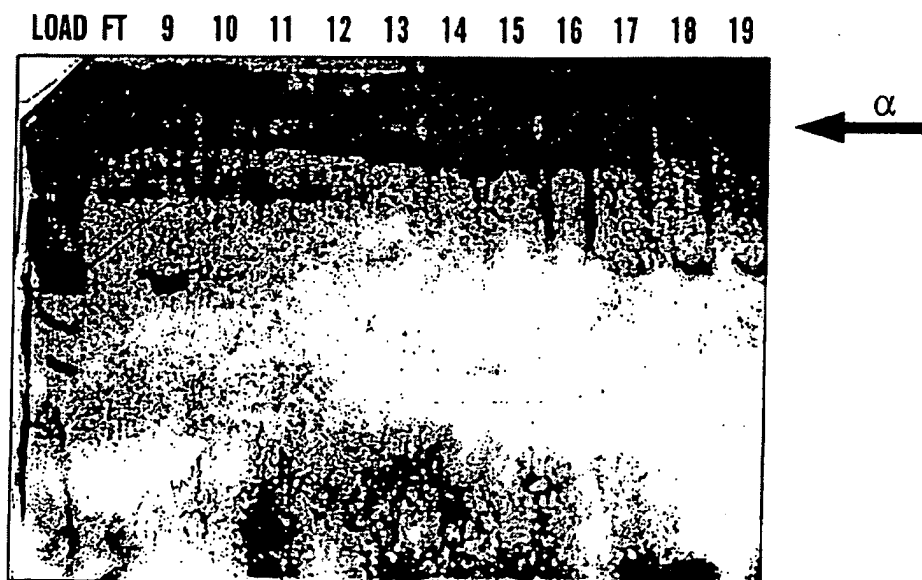


FIG. 14B

REPLACEMENT SHEET

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Alignment of TTH1 with alphas subunits of other organisms.

| | | | |
|---------|-------------------------------------|-----|---------|
| E.coli | DRYFLELIRTGRPDEESYLHAAVELAEARGLPVV | 197 | (ID#72) |
| V.chol. | DHFYLELIRTGRADEESYLHFALDVAEQYDLPVV | 197 | (ID#73) |
| H.inf. | DHFYALSRTGRPNEERYIQAAALKLAERCDLPLV | 197 | (ID#74) |
| R.prow. | DRFYFEIMRHDLP EEQFIENSYIQIASELSIPIV | 195 | (ID#75) |
| H.pyl. | DDFYLEIMRHGILDQRFIDEQVIKMSLETGLKII | 213 | (ID#76) |
| S.sp. | DDYYLEIQDHGSVEDRLVNINLVKIAQELDIKIV | 202 | (ID#77) |
| M.tub. | DNYFLELMDHGLTIERRVRDGLLEIGRALNIPPL | 220 | (ID#78) |
| T.th. | FFIEIQNHGLSEQK | | (ID#61) |

FIG. 15A

Alignment of TTH2 with alphas subunits of other organisms.

| | | | |
|---------|--|-----|---------|
| E.coli | NKRRAKNGEPPLDIAAIP LDDKKSFDM LQRSETTAVFQLESRGMKD | 618 | (ID#79) |
| V.chol. | NPRLKKAGKPPVRIEAIPLDDARSFRNLQDAKTTAVFQLESRGMKKE | 618 | (ID#80) |
| H.inf. | NVRMVREGKPRVDIAAIP LDDPESFELLKRSETTAVFQLESRGMKD | 618 | (ID#81) |
| R.prow. | CKLLKEQGIKIDFDDMTFDDKKTYQMLCKGKGVGVFQFESIGMKD | 624 | (ID#82) |
| H.pyl. | LKIITQHKISVDFLSLMDMDPKVYKTIQSGDTVGFQIES -GMFQ | 648 | (ID#83) |
| S.sp. | QERKALQIRARTGSKKLPDDVKKTHKLL EAGDLEGIFQLESQGMKQ | 643 | (ID#84) |
| M.tub. | IDNVRANRGIDLDESVP LDDKATYELLGRGDTLGVFQLDGGPMRD | 646 | (ID#85) |
| T.th. | RVELDYDALTLDD | | (ID#60) |

FIG. 15B

REPLACEMENT SHEET

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| | |
|--|------|
| ATGGGCCGGGAGCTCCGCTTCGCCCACCTCCACCAGCACA | |
| CCCAGTTCTCCCTCCTGGACGGGGCGGCGAAGCTTTCCGA | |
| CCTCCTCAAGTGGGTCAAGGAGACGACCCCGAGGACCCC | 120 |
| GCCTTGGCCATGACCGACCACGGCAACCTCTTCGGGGCCG | |
| TGGAGTTCTACAAGAAGGCCACCGAAATGGGCATCAAGCC | |
| CATCCTGGGCTACGAGGCCTACGTGGCGGCGGAAAGCCGC | 240 |
| TTTGACCGCAAGCGGGGAAAGGGCCTAGACGGGGGCTACT | |
| TTCACCTCACCCCTCCTCGCCAAGGACTTCACGGGGGTACCA | |
| GAACCTGGTGC GCCTGGCGAGCCGGGCTTACCTGGAGGGG | 360 |
| TTTTACGAAAAGCCCCGGATTGACCGGGAGATCCTGCGCG | |
| AGCACGCCGAGGGCCTCATCGCCCTCTCGGGGTGCCTCGG | |
| GGCGGAGATCCCCCAGTTCATCCTCCAGGACCGTCTGGAC | 480 |
| CTGGCCGAGGCCCGGCTCAACGAGTACCTCTCCATCTTCA | |
| AGGACCGCTTCTTCATCGAGATCCAGAACCACGGCCTCCC | |
| CGAGCAGAAAAAGGTCAACGAGGTCTCAAGGAGTTCGCC | 600 |
| CGAAAGTACGGCCTGGGGATGGTGGCCACCAACGACGGCC | |
| ATTACGTGAGGAAGGAGGACGCCCGCGCCACGAGGTCTCT | |
| CCTCGCCATCCAGTCCAAGAGCACCTTGGACGACCCCGGG | 720 |
| CGCTGGCGCTTCCCTGCGACGAGTTCTACGTGAAGACCC | |
| CCGAGGAGATGCGGGCCATGTTCCCGAGGAGGAGTGGGG | |
| GGACGAGCCCTTTGACAACACCGTGGAGATCGCCCGCATG | 840 |
| TGCAACGTGGAGCTGCCCATCGGGGACAAGATGGTCTACC | |
| GAATCCCCCGCTTCCCCCTCCCCGAGGGGCGGACCGAGGC | |
| CCAGTACCTCATGGAGCTCACCTTCAAGGGGCTCCTCCGC | 960 |
| CGCTACCCGGACCGGATCACCGAGGGCTTCTACCGGGAGG | |
| TCTTCCGCCTTTTGGGGAAGCTTCCCCCCCACGGGGACGG | |
| GGAGGCCTTGGCCGAGGCCTTGGCCCAGGTGGAGCGGGAG | 1080 |
| GCTTGGGAGAGGCTCATGAAGAGCCTCCCCCCTTTGGCCG | |
| GGGTCAAGGAGTGGACGGCGGAGGCCATTTTCCACCGGGC | |
| CCTTTACGAGCTTTCCGTGATAGAGCGCATGGGGTTTCCC | 1200 |
| GGCTACTTCCTCATCGTCCAGGACTACATCAACTGGGCCC | |
| GGAGAAACGGCGTCTCCGTGGGGCCCGGCAGGGGGAGCGC | |
| CGCCGGGAGCCTGGTGGCCTACGCCGTGGGGATCACCAAC | 1320 |
| ATTGACCCCTCCGCTTCGGCCTCCTCTTTGAGCGCTTCC | |
| TGAACCCGGAGAGGGTCTCCATGCCCGACATTGACACGGA | |
| CTTCTCCGACCGGGAGCGGGACCGGGTGATCCAGTACGTG | 1440 |
| CGGGAGCGCTACGGCGAGGACAAGGTGGCCCAGATCGGCA | |
| CCCTGGGAAGCCTCGCCTCCAAGGCCGCCCTCAAGGACGT | |
| GGCCCGGGTCTACGGCATCCCCCACAAGAAGGCGGAGGAA | 1560 |
| TTGGCCAAGCTCATCCCGGTGCAGTTCGGGAAGCCCAAGC | |
| CCCTGCAGGAGGCCATCCAGGTGGTGCCGGAGCTTAGGGC | |
| GGAGATGGAGAAGGACCCCAAGGTGCGGGAGGTCTTCGAG | 1680 |
| GTGGCCATGCGCCTGGAGGGCCTGAACCGCCACGCCTCCG | |
| TCCACGCCCGCGGGGTGGTGATCGCCGCCGAGCCCCTCAC | |
| GGACCTCGTCCCCCTCATGCGCGACCAGGAAGGGCGGCCC | 1800 |
| GTCACCCAGTACGACATGGGGGCGGTGGAGGCCTTGGGGC | |
| TTTTGAAGATGGACTTTTTGGGCCTCCGCACCCTCACCTT | |

FIG. 16A

REPLACEMENT SHEET

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| | |
|---|------|
| CCTGGACGAGGTCAAGCGCATCGTCAAGGCGTCCCAGGGG | 1920 |
| GTGGAGCTGGACTACGATGCCCTCCCCCTGGACGACCCCA | |
| AGACCTTCGCCCTCCTCTCCCGGGGGGAGACCAAGGGGGT | |
| CTTCCAGCTGGAGTCGGGGGGGATGACCGCCACGCTCCGC | 2040 |
| GGCCTCAAGCCGCGGCGCTTTGAGGACCTGATCGCCATCC | |
| TCTCCCTCTACCGCCCCGGGCCCATGGAGCACATCCCCAC | |
| CTACATCCGCGGCCACACGGGCTGGAGCCCGTGAGCTAC | 2160 |
| AGCGAGTTTCCCCACGCCGAGAAGTACCTAAAGCCCATCC | |
| TGGACGAGACCTACGGCATCCCCGTCTACCAGGAGCAGAT | |
| CATGCAGATCGCCTCGGCCGTGGCGGGGTACTCCCTGGGC | 2280 |
| GAGGCGGACCTCCTGCGGCGGTCCATGGGCAAGAAGAAGG | |
| TGGAGGAGATGAAGTCCCACCGGGAGCGCTTCGTCCAGGG | |
| GGCCAAGGAAAGGGGCGTGCCCGAGGAGGAGGCCAACCGC | 2400 |
| CTCTTTGACATGCTGGAGGCCTTCGCCAACTACGGCTTCA | |
| ACAAATCCCACGCTGCCGCCTACAGCCTCCTCTCCTACCA | |
| GACCGCCTACGTGAAGGCCCACTACCCCGTGGAGTTCATG | 2520 |
| GCCGCCCTCCTCTCCGTGGAGCGGCACGACTCCGACAAGG | |
| TGGCCGAGTACATCCGCGACGCCCGGGCCATGGGCATAGA | |
| GGTCCTTCCCCCGGACGTCAACCGCTCCGGGTTTGACTTC | 2640 |
| CTGGTCCAGGGCCGGCAGATCCTTTTCGGCCTCTCCGCGG | |
| TGAAGAACGTGGGCGAGGCGGCGGCGGAGGCCATTCTCCG | |
| GGAGCGGGAGCGGGGCGGCCCTACCGGAGCCTCGGCGAC | 2760 |
| TTCTCAAGCGGCTGGACGAGAAGGTGCTCAACAAGCGGA | |
| CCCTGGAGTCCCTCATCAAGGCGGGCGCCCTGGACGGCTT | |
| CGGGGAAAGGGCGCGGCTCCTCGCCTCCCTGGAAGGGCTC | 2880 |
| CTCAAGTGGGCGGCCGAGAACCAGGGAGAAGGCCCGCTCGG | |
| GCATGATGGGCCTCTTCAGCGAAGTGGAGGAGCCGCCTTT | |
| GGCCGAGGCCGCCCCCCCTGGACGAGATCACCCGGCTCCGC | 3000 |
| TACGAGAAGGAGGCCCTGGGGATCTACGTCTCCGGCCACC | |
| CCATCTTGCGGTACCCCGGGCTCCGGGAGACGGCCACCTG | |
| CACCTTGAGGAGCTTCCCCACCTGGCCCGGGACCTGCCG | 3120 |
| CCCCGGTCTAGGGTCTCCTTGCCGGGATGGTGGAGGAGG | |
| TGGTGCGCAAGCCCACAAAGAGCGGCGGGATGATGGCCCCG | |
| CTTCGTCTCTCCGACGAGACGGGGGCGCTTGAGGCGGTG | 3240 |
| GCATTCGGCCGGGCCTACGACCAGGTCTCCCCGAGGCTCA | |
| AGGAGGACACCCCCGTGCTCGTCTCGCCGAGGTGGAGCG | |
| GGAGGAGGGGGGCGTGCGGGTGCTGGCCCAGGCCGTTTGG | 3360 |
| ACCTACGAGGAGCTGGAGCAGGTCCCCCGGGCCCTCGAGG | |
| TGGAGGTGGAGGCCTCCCTCCTGGACGACCGGGGGGTGGC | |
| CCACCTGAAAAGCCTCCTGGACGAGCACGCGGGGACCCTC | 3480 |
| CCCCTGTACGTCCGGGTCCAGGGCGCCTTCGGCGAGGCC | |
| TCCTCGCCCTGAGGGAGGTGCGGGTGGGGGAGGAGGCTGT | |
| AGGCGGCCGCGTGGTTCCGGGCCTACCTCCTGCCCGACCG | 3600 |
| GGAGGTCTTTCTCCAGGGCGGCCAGGCGGGGGAGGCCAG | |
| GAGGCGGTGCCCTTCTAGGGGGTGCGCCGTGAGACCTAGC | |
| GCCATCGTTCTCGCCGGGGGCAAGGAGGCCTGGGCCCGAC | 3720 |
| CCCTTTTGG | |

FIG. 16B

REPLACEMENT SHEET

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| | |
|---|------|
| MGRELRF AHLHQHTQFSLLDGAPKLSDLLKWVEETTPEDP | |
| ALAMTDHGNLFGAVEFYKKATEMGIKPILGYEAYVAAESR | |
| FDRKRGKGLDGGYFHLTLLAKDFTGYQNLVRLASRAYLEG | 120 |
| FYEKPRIDREILREHAEGLIALSGLGAEIPQFILQDRLD | |
| LAEARLNEYLSIFKDRFFIEIQNHGLPEQKKVNEVLKEFA | |
| RKYGLGMVATNDGHYVRKEDARAHEVLLAIQSKSTLDDPG | 240 |
| ALALPCEEFYVKTPEEMRAMFPEEEVGGRSPLTTPWRSPH | |
| VORGAAIGTRWSTRI PRFPLPEGRTEAQYLMELTFKGLLR | |
| RYPDRITEGFIYREVFRLSGKLPPHGDGEALAEALAQVERE | 360 |
| AWERLMKSLPPLAGVKEWTAEAFHRLYELSAIERMGFP | |
| GLLPHRPGHLHQLGPEKGVSVGPGRGGAAGSLVAYAVGITN | |
| IDPLRFGLL FERFLNPERVSM PDIDTDFSDRERDRVIQYV | 480 |
| RERYGEDKVAQIGTLGSLASKAALKEVARVYGI PRKKAEE | |
| LAKLIPVQFGKPKPLQEA IQVPELRAEMEKDPKVREVL | |
| VAMRLEGLNRHASVHAGRGGVFSEPLTDLVPLCATRKGGP | 600 |
| YTQYDMGAVEALGLLKMDFLGLRTLTLFLDEVKRIVKASQG | |
| VELDYDALPLDDPKTFALLSRGETKGVFQLESGGMTATLR | |
| GLKPRRFEDLIAILSLYRPGPMEHIPTYIRRHHGLEPVSY | 720 |
| SEFPHAKEYLKPILDETYGIPVYQEQIMQIASAVAGYSLG | |
| EADLLRRSMGKKKVEEMKSHRERFVQAKERGVPEEEANR | |
| LFDMLEAFANYGFNKSHAAAYSLLSYQTAYVKAHYPVEFM | 840 |
| AALLSVERHDSKVAEYIRDARAMGIEVLPPDVNRSGFDF | |
| LVQGRQILFGLSAVKNVGEAAAAEAILRERERGGPYRSLGD | |
| FLKRLDEKVLNKRTLES LIKAGALDGFGERARLLASLEGL | 960 |
| LKWAAENREKARSGMMGLFSEVEEPPLAEAAPLDEITRLR | |
| YEKEALGIYVSGHPILRYPGLRETATCTLEELPHLARDLP | |
| PRSRVLLAGMVEEVVRKPTKSGGMMARFVLSDETGALEAV | 1080 |
| AFGRAYDQVSPRLKEDTPVLVLAEVEREEGGVRVLAQAVW | |
| TYQELEQVPRALEVEVEASLPDDRGV AHLKSLLDEHAGTL | |
| PLYVRVQGA FG EALLALREVRVGE EALGALEAAGFPAYLL | 1200 |
| PNREVSPRLTGSGGPRGRALSTGLALKTYPIALPGGNEAL | |
| ARPLL | |

FIG. 16C

REPLACEMENT SHEET

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| | | | | |
|----------|--|--------|--|--|
| | Start1 | Start2 | 3'-Exo I | |
| T.th. | VERVVRTLLDGRFLLEEGVGLWEWRYPPFLEGEAVVLDLETTGLAG-----LDEVIEVGLLRLEGG---RRLPF | | | |
| D.rad. | | | PWPQDVVDFDLETTGFSPA-----SAAIVEIGAVRIVGGQIDETLKF | |
| Bac.sub. | HGIKMIYGM EANLVDDGVPIAYNAAHRLLEEETVVFVDETGLSAV-----YDTIIELA AVKVKGGE--IIDKF | | | |
| H.inf. | | | MINPNRQIVLDTETTGMNQLGAHYEGHCHIEIGAVELINRR-YTGNNX | |
| E.c. | | | MSTAITRQIVLDTETTGMNQIGAHSEGHKIIIEIGAVEVVNRR-LTGNNF | |
| H.pyl. | NLEYLKACGLNFIETSENLI TLKNLKTPLKDEVFSFIDLETTGSCPI-----KHEILEIGAVQVKGE--IINRF | | | |
| | | | 3'-Exo II | |
| T.th. | QSLVR-PLPP---AEARSWNL T---GIPREALEEAPSLEEVLEKAYPLRGDATLVIHNAAFDLGFL-RPALEGLG | | | |
| D.rad. | ETLVR-PTRPDGSML SIPWQAQRVHGISDEMVRRAPAXKDVLPDFDFVDGS AVVAHNVSFDGGFM-RAGAERLG | | | |
| Bac.sub. | EAFAN-PHRP---LSATIIELT---GITDDMLQADPDVVDVIRDFREWIGDDILVAHNASFDMGFL-NVAYKKLL | | | |
| H.inf. | HIYIK-PDRP---XDPDAIKVH---GITDEMLADKPEFKEVAQDFLDYINGAELLIHNAFPDVGFM-DYEFKRKLN | | | |
| E.c. | HVYIK-DRLV---DPEAFGVH---GIAVDFLDKPTFAEVAVEFMDYIRGAELV IHNAAFDVGFM-DYEFSLLK | | | |
| H.pyl. | ETLVKVKSV P-----DYIAELT---GITYEDTLNAPSAHEALQELRLFLGNSV FVAHNANFDYNFLGRYFVEKLLH | | | |
| | | | 3'-Exo III | |
| T.th. | -----YRLENPVVDSLRLARRGLPGLRRYGLDALSEVLELPRRT--CHRALEDVERTLAVVHEVYMLT-----SG | | | |
| D.rad. | -----LSWAPERELCTMQLSRRAPPRERTHNLTVLAERLGLFAPGGRHRSYGDVQVTAQAYLRLLLELLG-----ER | | | |
| Bac.sub. | E-----VEKAKNPVIDTLELGRFLYPEFKNHRLNTLCKKFDIELTQ--HHRAIYDTEATAYLLKMLKDA-----EK | | | |
| H.inf. | -LNVKTDDICLVTDTLQMARQMPGKRN-NLDALCDRLGIDNSKRTLHGALLDAEILADVYLMMTGGQTNLFDEEE | | | |
| E.c. | RDI AKTNFTCKVTDLSLAVARKMFPGKRN-SLDALCARYEIDNSKRTLHGALLDAQILAEVYLAMTGGQTSMAFAME | | | |
| H.pyl. | -----CPLLNLKLC TDL SKRAILSMRY-SLSFLKELLGFGIEV--SHRAYADALASYKLF EICLLNLP--SYIKT | | | |

FIG. 17

REPLACEMENT
SHEET

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ATGGTGGAGCGGGTGGTGC GGACCCTTCTGGACGGGAGGT 40
TCCTCCTGGAGGAGGGGGTGGGGCTTTGGGAGTGGCGCTA
CCCCTTTCCCCTGGAGGGGGAGGCGGTGGTGGTCCTGGAC 120
CTGGAGACCACGGGGCTTGCCGGCCTGGACGAGGTGATTG
AGGTGGGCCTCCTCCGCCTGGAGGGGGGAGGCGCCTCCC 200
CTTCCAGAGCCTCGTCCGGCCCCCTCCCGCCCGCCGAAGCC
CGTTCGTGGAACCTCACCGGCATCCCCCGGGAGGCCCTGG 280
AGGAGGCCCCCTCCCTGGAGGAGGTTCTGGAGAAGGCCTA
CCCCCTCCGCGGCGACGCCACCTTGGTGATCCACAACGCC 360
GCCTTTGACCTGGGCTTCCTCCGCCCCGGCCTTGGAGGGCC
TGGGCTACCGCCTTGAAAACCCCGTGGTGGACTCCCTGCG 440
CTTGGCCAGACGGGGCTTACCAGGCCTTAGGCGCTACGGC
CTGGACGCCCTCTCCGAGGTCCTGGAGCTTCCCCGAAGGA 520
CCTGCCACCGGGCCCTCGAGGACGTGGAGCGCACCCCTCGC
CGTGGTGCACGAGGTATACTATATGCTTACGTCCGGCCGT 600
CCCCGCACGCTTTGGGAACTCGGGAGGTAG

FIG. 18A

MVERVVRTL LDGRFLLEEGVGLWEWRYPFPLEGEAVVLD 40
LETTGLAGLDEVIEVGLLRLEGGRRLPFQSLVRPLPPAEA
RSWNLTGIPREALEEAPSLEEVLEKAYPLRGDATLVIHNA 120
AFDLGFLRPALEGLGYRLENPVVDSLRLARRGLPGLRRYG
LDALSEVLELPRRTCHRALEDVERTLAVVHEVYYMLTSGR 200
PRTLWELGRZ

FIG. 18B

REPLACEMENT
SHEET

Alignment of dnaA genes.

| | | | | | | | |
|----------|-----------------|------------------|-----------------|-----------------|-----------------|------------------|-----|
| P. mar. | MLEASWEK | VQSSL--KQNLK-- | -----PSYE | TWIRPTEFSG--FKN | GELTLIAPNSFSSAW | LKNYSQTIQETAE- | 65 |
| Syn. sp. | MVSCENLWQQ | ALAIL--ATQLTK-- | -----PAFD | TWIKASVLIS--LGD | GVATIQVENGFVLNH | LQKSYGPLLMEVLT- | 67 |
| B. sut. | MENILDWNQ | ALAI--EKKLSK-- | -----PSFE | TWMKSTKAHS--LQG | DTLTITAPNEFARDW | LESRYLHLIADTIY- | 67 |
| M. tub. | MTDDPGSGFTTVWNA | VVSELNGDPKVDDGP | SSDANLSAPLTPQQR | AWNLVQPLT--IVE | GFALLSVPSFVQNE | IERHLRAPITDALS- | 87 |
| T. th. | MSHEAVWQH | VLEHI--RRSITE-- | -----VEFH | TWFERIRPLG--IRD | GVLEAVPTSFALDW | IRHYAGLIQEGPR- | 66 |
| E. coli | MSLSLWQQ | CLARL--QDELPA-- | -----TEFS | MMIRPLQAE--LSD | NTLALYAPNRFVLDW | VRDKYLNNINGLLT- | 64 |
| T. mar. | MKER | ILQEI--KTRVNR-- | -----KSWE | LWFSDFVKS--IEG | NKVVSFVGNLFIKEW | LEKKYYSVLKAVK- | 61 |
| H. pyl. | MDTNNNIEKE | ILALVKQNPKVSL-- | -----IEYE | NYFSQLKYNPNASKS | DIAPFVAPNQVLCTT | ITAKYGALLKEILSQ | 72 |
| P. mar. | EIFG--- | EPVTVHVK | VKANAESSDEHYSSA | P----- | ITPPLASPGSV | DSSGSSLRLSK---- | 130 |
| Syn. sp. | DLTG--- | QEITVKLI | TDGLEPHS---- | LIGQ | E----- | SSLPMETTP---- | 115 |
| B. sut. | ELTG--- | EELSIFV | IPQNDVEDFMPKPQ | VKKAVKEDTSDFPQN | ----- | ----- | 119 |
| M. tub. | RRLGH-QIQLGVRIA | PPATDEADDTTVPPS | ENPATTSPDTTDDND | EIDDSAAARGDNQHS | WPSYFTERPHNTDSA | TAGVTSLNRRYTFDT | 176 |
| T. th. | LLGAQ-APRFELRVV | PGVVQEDIFQPPPS | PPAQAP----- | ----- | ----- | -----EDTFKT | 108 |
| E. coli | SFCGADAPQLRFEVG | TKPVTQTPQAAVTSN | VAAPAQVAQTQPQRA | APSTRSGWNVVAPA | EP----- | -TYRSNVNVKHTFDN | 140 |
| T. mar. | VVLG--- | NDATFEIT | YEAFEPHSSYSEPLV | KKRAVLLTP----- | ----- | -----LNPDYTFEN | 106 |
| H. pyl. | NKVG-MHLAHSVDVR | IEVAPKIQINAQSN | NYKAIKTS----- | ----- | ----- | -----VKDSYTFEN | 118 |
| P. mar. | FVVGPNRMAHAAAM | AVAESPGREFNPLFI | CGGVGLGKTHLMQAI | GHYRLEIDPGAKVSY | VSTETFTNDLIL--A | IRQDRMQAFDRYR- | 217 |
| Syn. sp. | FVVGPTNRMAHAASL | AVAESPGREFNPLFL | CGGVGLGKTHLMQAI | AHYRLEMYPNNAKVY | VSTERFTNDLIT--A | IRQDNMEDFRSYR- | 202 |
| B. sut. | FVIGSGNRFAHAASL | AVAEAPAKAYNPLFI | YGGVGLGKTHLMHAI | GHYVIDHNPNAKVY | LSSEKFTNEFIN--S | IRDNKAVDFRNRYR- | 206 |
| M. tub. | FVIGASNRFAHAASL | AIAEAPARAYNPLFI | WGESGLGKTHLLHAA | GNVYQRLFPGRVRY | VSTEEFTNDFIN--S | LRDRKVAFRKRSYR- | 263 |
| T. th. | SMWGPTTPWPHGGAV | AVAESPGRAYNPLFI | YGGRLGKTYLMLHAV | GPLRAKRFPHMRLEY | VSTETFTNELINRPS | AR-DRMTEFRERYR- | 196 |
| E. coli | FVEGKSNQLARAAAR | QVADNPGGAYNPLFL | YGGTGLGKTHLLHAV | GNGIMARKPNNAKVY | MHSERFVQDMVK--A | LQNNAIIEEFKRYR- | 227 |
| T. mar. | FVVGPGNSFAYHAAL | EVAKHPGR--YNPLFI | YGGVGLGKTHLLQSI | GNVYVQNEPDLRVMY | ITSEKFLNDLVD--S | MKEGKLNFEFREKYR | 193 |
| H. pyl. | FVVGSCNNTVYEIAK | KVAQSDTPPPYNPLV | YGGTGLGKTHILNAI | GNHALEK--HKKVVL | VTSEDFLTDFLK--H | LDNKTMTDSFKAKYR- | 203 |

FIG. 19A

REPLACEMENT SHEET

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| | | | | | | | |
|----------|------------------|------------------|------------------|------------------|------------------|-----------------|-----|
| P. mar. | AADLILVDDIQFIEG | KEYTQEEFFHTFNAL | HDAGSQIVLASDRPP | SQIPRLQERLMSRFS | MGLIADVQAPDLETR | MAILQKKAHERVGL | 307 |
| Syn. sp. | SADFLILDDIQFIKG | KEYTQEEFFHTFNAL | HEAGQWVASDRAP | QRIPLQDRRLISRFS | MGLIADIQVPDLETR | MAILQKKAEDRIRL | 292 |
| B. sut. | NVDVLLDDIQFLAG | KEQTQEEFFHTFNAL | HEESKQIVISSDRPP | KEIPTLEDRLRSRFE | WGLITDITPPDLETR | TAILRKKAKAEGLDI | 296 |
| M. tub. | DVDVLLVDDIQFIEG | KEGIQEEFFHTFNAL | HNANKQIVISSDRPP | KQATLEDRLRTRFE | WGLITDVQPPPELETR | TAILRKKAQMERLAV | 353 |
| T. th. | SVDLLLVDDVQFIAG | KERTQEEFFHTFNAL | YEAHKQIILSSDRPP | KDILTLEARLRSRFE | WGLITDNPAAPDLETR | TAILKMNAS-SCPED | 285 |
| E. coli | SVDALLIDDDIQFFAN | KERSQEEFFHTFNAL | LEGNQIILTSDRYP | KEINGVEDRLKSRFG | WGLTVAIPEPPELETR | VAILMKKADENDIRL | 317 |
| T. mar. | KVDILLLDDVQFLIG | KTGVQTELFHTFNEL | HDSGQIIVICSDREP | QKLSEFQDRLVSRFQ | MGLVAKLEPPDEETR | KSIARKMLEIEHGEL | 283 |
| H. pyl. | HCDFLLDDAQFLQG | KPKLEEEFFHTFNEL | HANSKQIVLISDRSP | KNIAGLEDRLKSRFE | WGITAKVMPDLETK | LSIVKQKQCLNQITL | 293 |
| P. mar. | PRDLIQFIACRFTSN | IRELEGALTRAIAFA | SITGLPMTVDSIAPM | LD-----PNGQVEVT | PKQVLDKVAEVFKVT | PDEMRSASRRR-PVS | 392 |
| Syn. sp. | PKEVIEYIASHVTSN | IREGALIRAIAYT | SLSNVAMTVENIAPV | LN-----PPVEKVAAA | PETIITIVAQHYQLK | VEELLSNSRRR-EVS | 377 |
| B. sut. | PNEVMLYIANQIDSN | IREGALIRVWAYS | SLINKDINADLAAEA | LKDII-PSSKPKVIT | IKEIQRVVGQQFNK | LEDFKAKKRTK-SVA | 384 |
| M. tub. | PDDVLELIAASSIERN | IREGALIRVTAF | SLANKTPIDKALAEIV | LRDLI-ADANTMQIS | AATIMAATAEYFDYT | VEELRGPGKTR-ALA | 441 |
| T. th. | PEDALEYIARQVTSN | IREWEGALMRASPFA | SLNGVELTRAVAACA | LRHLR-P--RELEAD | PLEIIRKKAAGPVRPE | TPGGAHGERRKKEW | 372 |
| E. coli | PGEVAFFIAKRLRSN | VRELEGALNRVIANA | NFTGRAITIDFVREA | LRDLL-A-LQEKLV | IDNIOKTVAEYKIK | VADLLSKRRSR-SVA | 404 |
| T. mar. | PEEVNLFVAENVDDN | LRRLRGAIKLLVYK | ETTQKEVDLKEAILL | LKDFIKPNRVKAMD | IDELIEIVAKVTGVP | REEILSNSRV-KAL | 372 |
| H. pyl. | PEEVMEYIAQHISDN | IRQMEGAIKISVNA | NLMNASIDLNLAKTV | LEDL--QKDHAEGSS | LENILLAVAQSLNLK | SSEIKVSSRQK-NVA | 380 |
| P. mar. | QARQVGMVLMRQGTN | LSLPRIGDTFGGKDH | TTVMYAIEQVEKKLS | S-----DPQIA | SQVQKIRDLLQIDSR | RKR----- | 461 |
| Syn. sp. | LARQVGMVLMRQHTD | LSLPRIGEAFGGKDH | TTVMYSCDKITQLQQ | K-----DWETS | QTLTSLSHRINIAGQ | APES----- | 447 |
| B. sut. | FPRQIAMVLSREMTD | SSLPKIGEEFFGGRDH | TTVVIHAHEKISKLLA | D-----DEQLQ | QHVKEIKEQLK---- | ----- | 446 |
| M. tub. | QSRQIAMVLCRELTD | LSLPKIGQAFG-RDH | TTVMYAQRKILSEMA | E-----RREVF | DHVKELTTRIRQRSK | R----- | 507 |
| T. th. | LPRQLAMVLVRELTP | ASLPEIGQLFGGRDH | TTVRYAIQKVQELAG | KP-----DREVQ | GLLRTLREACTDPVD | NLWITCG | 446 |
| E. coli | RPRQMAMALAKELTN | HSLPEIGDAFGGRDH | TTVLHACRKIEQLRE | E-----SHDIK | EDFSNLIRTLSS---- | ----- | 467 |
| T. mar. | TARRIGMYVAKNYLK | SSLRTIAEKFN-RSH | PVVVDSVKVKVDSLL | KG-----NKQLK | ALIDEVIGEISRRAL | SG----- | 440 |
| H. pyl. | LARKLVVYFARLYTP | NPTLSLAQFLDLKDH | SSISKMYSGVKMME | EEKSPFVLSLREEIK | NRLNELNDKKTAFNS | SE----- | 457 |

FIG. 19B

REPLACEMENT
SHEET

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GTGTCGCACGAGGCCGTCTGGCAACACGTTCTGGAGCACA
TCCGCCGCAGCATCACCGAGGTGGAGTTCCACACCTGGTT
TGAAAGGATCCGCCCCCTTGGGGATCCGGGACGGGGTGCTG 120
GAGCTCGCCGTGCCCACCTCCTTTGCCCTGGACTGGATCC
GGCGCCACTACGCCGGCCTCATCCAGGAGGGCCCTCGGCT
CCTCGGGGCCCAGGCGCCCCGGTTTGAGCTCCGGGTGGTG 240
CCCGGGGTCGTAGTCCAGGAGGACATCTTCCAGCCCCCGC
CGAGCCCCCGGCCCAAGCTCAACCCGAAGATACCTTTAA
AACTTCGTGGTGGGGCCCAACAACCTCCATGGCCCCACGGC 360
GGCGCCGTGGCCGTGGCCGAGTCCCCCGGCCGGGCCTACA
ACCCCTCTTCATCTACGGGGGCGGTGGCCTGGGAAAGAC
CTACCTGATGCACGCCGTGGGCCCCTCCGTGCGAAGCGC 480
TTCCCCCACATGAGATTAGAGTACGTTTCCACGGAACTT
TCACCAACGAGCTCATCAACCGGCCATCCGCGAGGGACCG
GATGACGGAGTTCCGGGAGCGGTACCGCTCCGTGGACCTC 600
CTGCTGGTGGACGACGTCCAGTTCATCGCCGGAAAGGAGC
GCACCCAGGAGGAGTTTTTCCACACCTTCAACGCCCTTTA
CGAGGCCCAACAAGCAGATCATCCTCTCCTCCGACCGGCCG 720
CCCAAGGACATCCTCACCTGGAGGCGCGCCTGCGGAGCC
GCTTTGAGTGGGGCCTGATCACCGACAATCCAGCCCCCGA
CCTGGAAACCCGGATCGCCATCCTGAAGATGAACGCCAGC 840
AGCGGGCCTGAGGATCCCGAGGACGCCCTGGAGTACATCG
CCCGGCAGGTCACCTCCAACATCCGGGAGTGGGAAGGGGC
CCTCATGCGGGCATCGCCTTTCGCCCTCCCTCAACGGCGTT 960
GAGCTGACCCGCGCCGTGGCGGCCAAGGCTCTCCGACATC
TTCGCCCCAGGGAGCTGGAGGCGGACCCCTTGGAGATCAT
CCGCAAAGCGGCGGGACCAGTTCGGCCTGAAACCCCGGGA 1080
GGAGCTCACGGGGAGCGCCGCAAGAAGGAGGTGGTCCTCC
CCCGGCAGCTCGCCATGTACCTGGTGCGGGAGCTCACCCC
GGCCTCCCTGCCCGAGATCGACCAGCTCAACGACGACCGG 1200
GACCACACCACGGTCCTCTACGCCATCCAGAAGGTCCAGG
AGCTCGCGGAAAGCGACCGGGAGGTGCAGGGCCTCCTCCG
CACCTCCGGGAGGCGTGCACATGA

FIG. 20A

REPLACEMENT
SHEET

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VSHEAVWQHVLEHIRRSITEVEFHTWFERIRPLGIRDGVL
ELAVPTSFALDWIRRHAYAGLIQEGPRLPGAQAPRFELRVV
PGVVVQEDIFQPPPSPPAQAPEDTFKTSWWGPTTPWPHG 120
GAVAVAESPGRAYNPLFIYGGRGLGKTYLMHAVGPLRAKR
FPHMRLEYVSTETFTNELINRPSARDRMTEFRERYRSVDL
LLVDDVQFIAGKERTQEEFFHTFNALYEAHKQIILSSDRP 240
PKDILTLEARLRSRFEWGLITDNPAPDLETRAILKMNAS
SGPEDPEDALEYIARQVTSNIREWEGALMRASPFASLNGV
ELTRAVAAKALRHLRPRELEADPLEIIRKAAGPVRPETPG 360
GAHGERRKKEVVLPRQLAMYLVLRELTPASLPEIDQLNDDR
DHTTVLYAIOKVQELAESDREVQGLLRTLREACT

FIG. 20B

REPLACEMENT
SHEET

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ATGAACATAACGGTTCCCAAAAACTCCTCTCGGACCAGC 40
TTTCCCTCCTGGAGCGCATCGTCCCCTCTAGAAGCGCCAA
CCCCCTCTACACCTACCTGGGGCTTTACGCCGAGGAAGGG 120
GCCTTGATCCTCTTCGGGACCAACGGGGAGGTGGACCTCG
AGGTCCGCCTCCCCGCCGAGGCCCAAAGCCTTCCCCGGGT 200
GCTCGTCCCCGCCAGCCCTTCTTCCAGCTGGTGCGGAGC
CTTCCTGGGGACCTCGTGGCCCTCGGCCTCGCCTCGGAGC 280
CGGGCCAGGGGGGGCAGCTGGAGCTCTCCTCCGGGCGTTT
CCGCACCCGGCTCAGCCTGGCCCCTGCCGAGGGCTACCCC 360
GAGCTTCTGGTGCCCCGAGGGGGAGGACAAGGGGGCCTTCC
CCCTCCGGACGCGGATGCCCTCCGGGGAGCTCGTCAAGGC 440
CTTGACCCACGTGCGCTACGCCGCGAGCAACGAGGAGTAC
CGGGCCATCTTCCGCGGGGTGCAGCTGGAGTTCTCCCCC 520
AGGGCTTCCGGGCGGTGGCCTCCGACGGGTACCGCCTCGC
CCTCTACGACCTGCCCCTGCCCCAAGGGTTCCAGGCCAAG 600
GCCGTGGTCCCCGCCCGGAGCGTGGACGAGATGGTGCGGG
TCCTGAAGGGGGCGGACGGGGCCGAGGCCGTCCTCGCCCT 680
GGGCGAGGGGGTGTTGGCCCTGGCCCTCGAGGGCGGAAGC
GGGGTCCGGATGGCCCTCCGCCTCATGGAAGGGGAGTTCC 760
CCGACTACCAGAGGGTCATCCCCCAGGAGTTCGCCCTCAA
GGTCCAGGTGGAGGGGGAGGCCCTCAGGGAGGCGGTGCGC 840
CGGGTGAGCGTCCTCTCCGACCGGCAGAACCACCGGGTGG
ACCTCCTTTTGGAGGAAGGCCGGATCCTCCTCTCCGCCGA 920
GGGGGACTACGGCAAGGGGCAGGAGGAGGTGCCCCGCCAG
GTGGAGGGGCGGACATGGCCGTGGCCTACAACGCCCGCT 1000
ACCTCCTCGAGGCCCTCGCCCCCGTGGGGGACCGGGCCCA
CCTGGGCATCTCCGGGCCCACGAGCCCGAGCCTCATCTGG 1080
GGGGACGGGGAGGGGTACCGGGCGGTGGTGGTGCCCTCA
GGGTCTAG 1128

FIG. 21A

REPLACEMENT
SHEET

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MNITVPKKLLSDQLSLLERIVPSRSANPLYTYLGLYAEEG 40
ALILFGTNGEVDLEVRPAEAQSLPRVLVPAQPFFQLVRS
LPGDLVALGLASEPGQGQLELSSGRFRTRLAPAEGLYP 120
ELLVPEGEDKGAFPLRTRMPGELVKALTHVRYAASNEEY
RAIFRGVQLEFSPQGFRAVASDGYRLALYDLPLPQGFQAK 200
AVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALEGGS
GVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVR 280
RVSVLSDRQNHVRVDLLLEEGRILLSAEGDYGKGQEEVPAQ
VEGPDMAVAYNARYLLEALAPVGDRAHLGISGPTSPSLIW 360
GDGEGYRAVVVPLRVZ

FIG. 21B

REPLACEMENT SHEET

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| | |
|--------------|---|
| T. th. beta | MNITVPKLLSDQLSLERIVPSRSANPLYTYLGLYAEAGALILFGTNGEVDLEVRPAE |
| E. coli. bet | MKFTVEREHLKPLQOVSGPLGGRPTLPILGNLLQVADGTLSTLGTDLMEMVARVALV |
| P. mirab. be | MKFIIEREQLKPLQOVSGPLGGRPTLPILGNLLKVTENTLSTLGTDLMEMMARVSL |
| H. infl. bet | MQFSISRENLLKPLQOVCGVLSNRPNIPVLNNVLLQIEDYRLTITGTDLLEVELSSQTQLS |
| P. put. beta | MHFTIQREALKPLQLVAGVVERQTLPVLSNVLVQGGQQLSTLGTDLLEVELVGRVQLE |
| B. cap. beta | MKFTIQNDILTGNLKKITRVLVKNISFPILNLIQVEDGTLSTTTNLEIELISKIEII |
| | * * |
| T. th. beta | AQSLP-RVLVPAQPFQVLVRSPLGDLVALGLASEPGQGQLELSSGRFRTRLSLAPAEY |
| E. coli. bet | QPEPGATTVPARKFFDICRGLP-EGAEIAVQLE--GERMLVRSGRSRSFSLSTLPAADF |
| P. mirab. be | QSHGIGATTVPARKFFDIWRGLP-EGAEISVELD--GDRLLVRSGRSRSFSLSTLPAADF |
| H. infl. bet | SSSENGTFTIPAKKFLDICRTLS-DDSEITVTFE--QDRALVQSGRSRFTLATQPAEY |
| P. put. beta | EPAEPGEITVPARKLMDICKSLP-NDALIDIKVD--EQKLLVKAGRSRFTLSTLPANDF |
| B. cap. beta | TKYIPGKTTISGRKILNICRTLS-EKSKIKMQLK--NKKMYISSENSNYILSTLSADTF |
| | * * |
| T. th. beta | PELLVPEGEDKGAFPLRTRMPSGELVKALTHVRYAASNEEYRAIFRGVQLEFSQQFRAV |
| E. coli. bet | PNLDD--WQSEVEFTLPQAT----MKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTV |
| P. mirab. be | PNLDD--WQSEVEFTLPQAT----LKRLIESTQFSMAHQDVRYYLNGMLFETEGEELRTV |
| H. infl. bet | PNLTD--WQSEVDFELPQNT----LRRLIEATQFSMANQDARYFLNGMKFETEGNLLRTV |
| P. put. beta | PTVEE--GPGSLTCNLEQSK----LRRLIERTSFAMAQQDVRYYLNGMLLEVSRLTLRAV |
| B. cap. beta | PNHQN--FDYISKFDISSNI----LKEMIEKTEFSMGKQDVRYYLNGMLLEKKDKFLRSV |
| | * * |
| T. th. beta | ASDGYRLALYDLPLPQGFQA--KAVVPARSVDENVRLKGADGAEAVLAGEVLALE |
| E. coli. bet | ATDGHRLAVCSMPIGQSLPS-HSVIVPRKGVIELMRMLDG-GDNPLRVQIGSNNIRAHVG |
| P. mirab. be | ATDGHRLAVCAMDIGQSLPG-HSVIVPRKGVIELMRMLDGSGESLLQLQIGSNNIRAHVG |
| H. infl. bet | ATDGHRLAVCTISLEQELQN-HSVILPRKGVLELVRLLLET-NDEPARLQIGTNNLRVHLK |
| P. put. beta | STDGHRLALCMSAPIEQEDRHQVIVPRKGILELARLLTD-PEGMVSVIVLQGHHRATG |
| B. cap. beta | ATDGYRLAISYTQLKKDINF-FSIIIPNKAVMELLKLLNT-QPQLLNILIGSNSIRIYTK |
| | .. ** *** * |

FIG. 22A

REPLACEMENT SHEET

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| | | |
|--------------|--|----------|
| T. th. beta | GGSGVRMALRMEGEFPDYQYRVIPOEFALKVQVEGEALREAVRRVSVLSDRQHRVDLLL | |
| E. coli. bet | ---DFIFTSKLV DGRFPDYRRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLVY | |
| P. mirab. be | ---DFIFTSKLV DGRFPDYRRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLVY | |
| H. infl. bet | ---NTVFTSKLIDGRFPDYRRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLVY | |
| P. put. beta | ---EFTFTSKLV DGRFPDYRRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLVY | |
| B. cap. beta | ---NLIFTTQLIEGEYPDYKSVLFKEKNPIITNSILLKKSLLRVAILAHEKFCGIEIKI | |
| | * . . . * . . . * . . . * . . . * | |
| T. th. beta | EEGRILLSAEGDYCK - GQEEVPAQVEGPDMAVAYNARYLLEALAPVG - DRAHLGISGPTS | |
| E. coli. bet | SENQLKITANNPEQEEAEIILDVTSYSGAEIEIGFNVSYYLDVNLKALCENVRMMLTDSVS | |
| P. mirab. be | TNGQLKITANNPEQEEAEIIVDVQYQGEEMEIGFNVSYYLDVNLKALCENVRMMLTDSVS | |
| H. infl. bet | KENQLKITASNTHEHEEAEIIVDVNNGEELVGFNVYIILDVNLKALCENVRMMLTDSVS | |
| P. put. beta | AAGQLKIQANNPEQEEAEIISVDYEGSSLEIGFNVSYYLDVNLKALCENVRMMLTDSVS | |
| B. cap. beta | ENGKFKVLSDNQEEETAEDLFEIDYFGEKIEISINVVYLLDVINNICKSENIALFLNKS | |
| | * . . . * . . . * . . . * . . . * | |
| T. th. beta | PSLIWGDG - EGYRAVVVPLRVZ | (ID#108) |
| E. coli. bet | SVQIEDAASQSAAYVVMMPMRLZ | (ID#109) |
| P. mirab. be | SVQVENVASAAAAAYVVMMPMRL - | (ID#110) |
| H. infl. bet | SCLIENCEDSSCEYVIMPMRL - | (ID#111) |
| P. put. beta | SALLQEAAGNDSSSYVVMMPMRL - | (ID#112) |
| B. cap. beta | SIQIEAENSSNAYVVMMLLKR - | (ID#113) |
| | * . . . * | |

FIG. 22B

REPLACEMENT
SHEET

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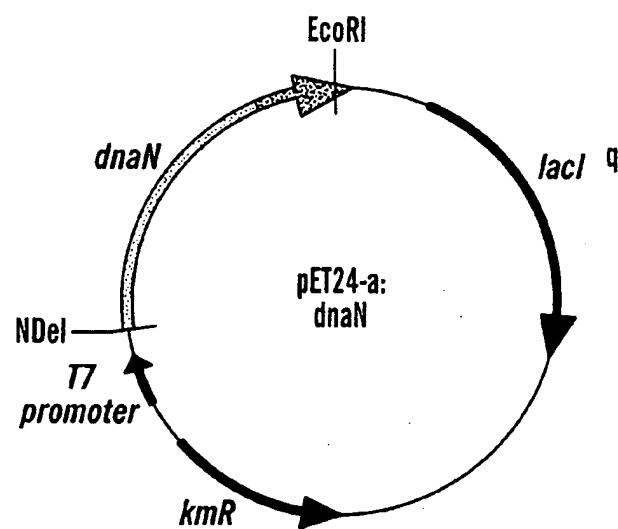


FIG. 23

REPLACEMENT
SHEET

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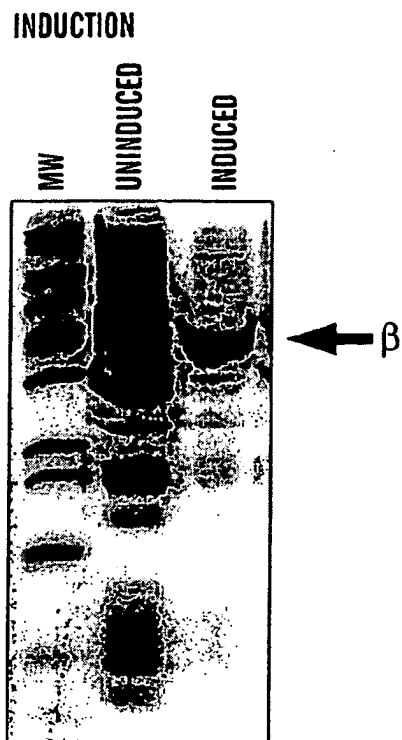


FIG. 24A

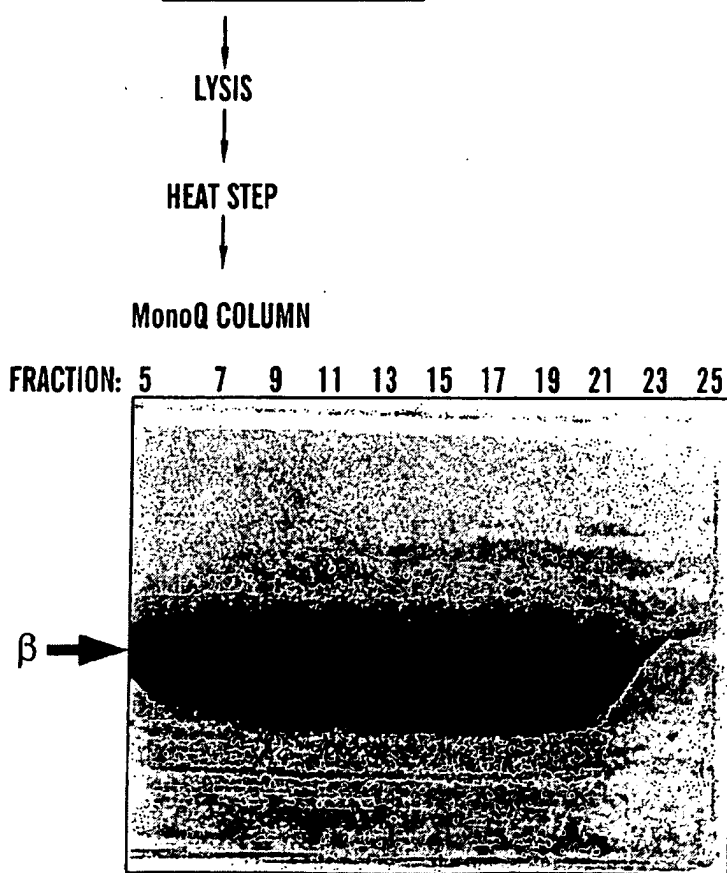


FIG. 24B

REPLACEMENT
SHEET

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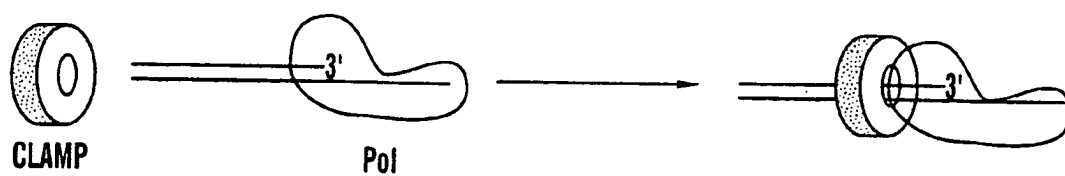


FIG. 25A

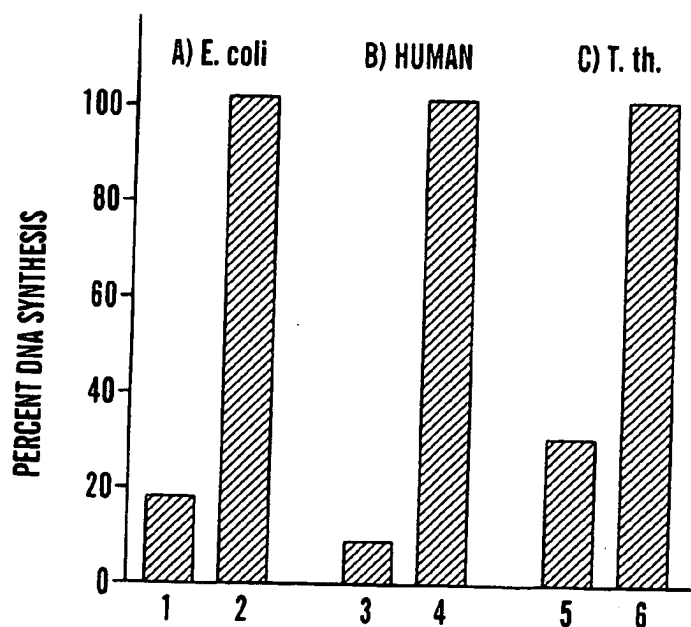


FIG. 25B

REPLACEMENT
SHEET

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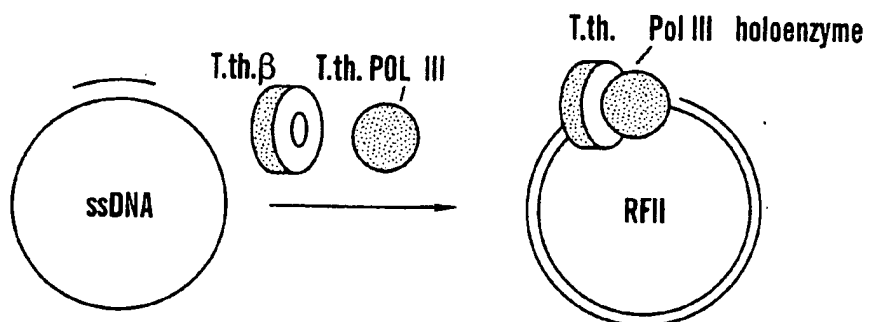


FIG. 26A

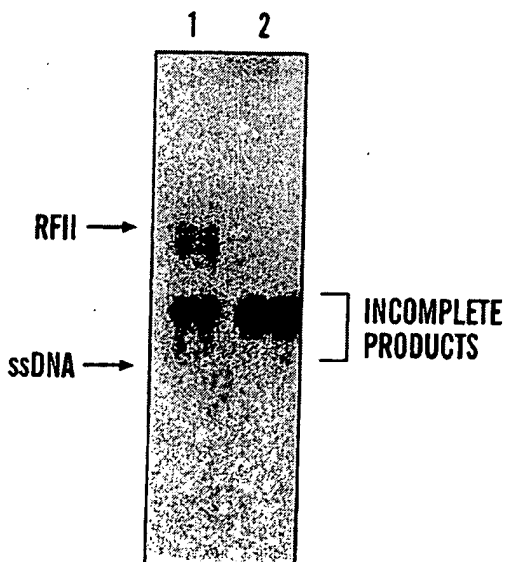


FIG. 26B

REPLACEMENT SHEET

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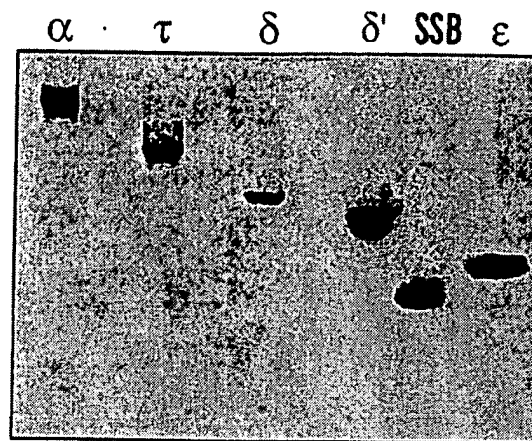


FIG. 27

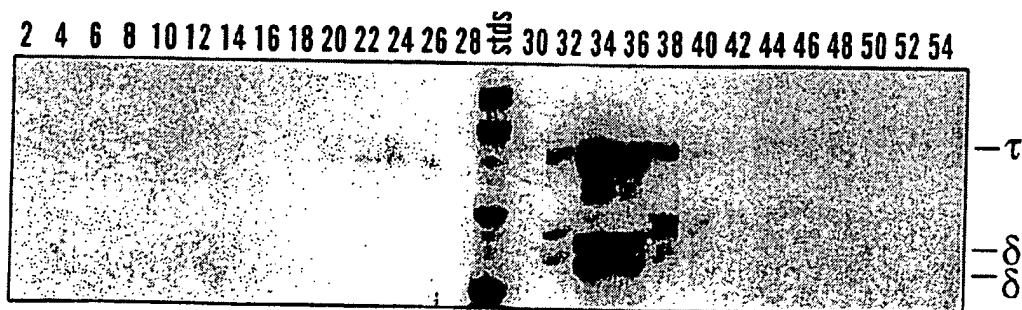


FIG. 28

REPLACEMENT SHEET

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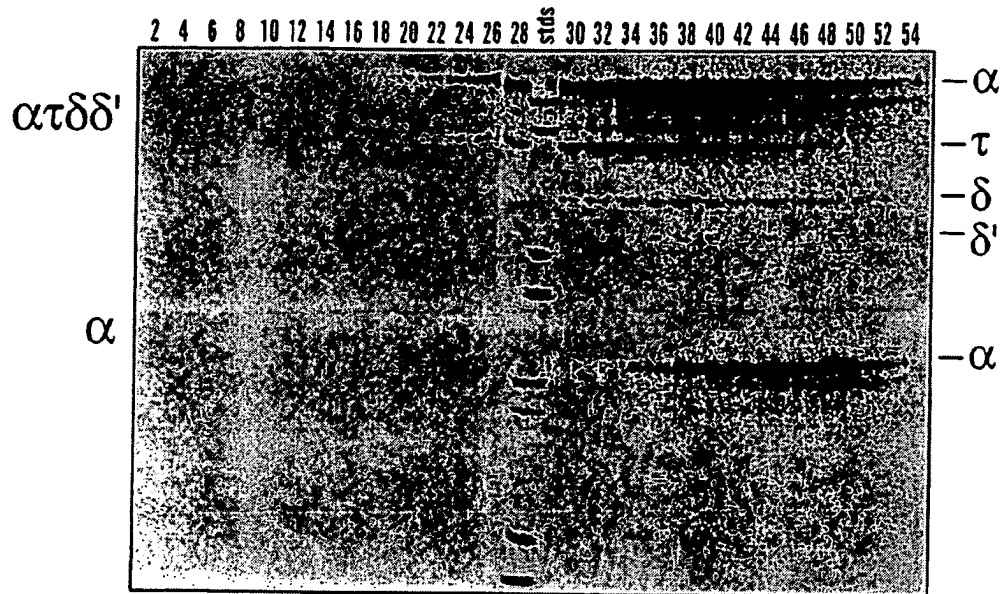


FIG. 29

REPLACEMENT
SHEET

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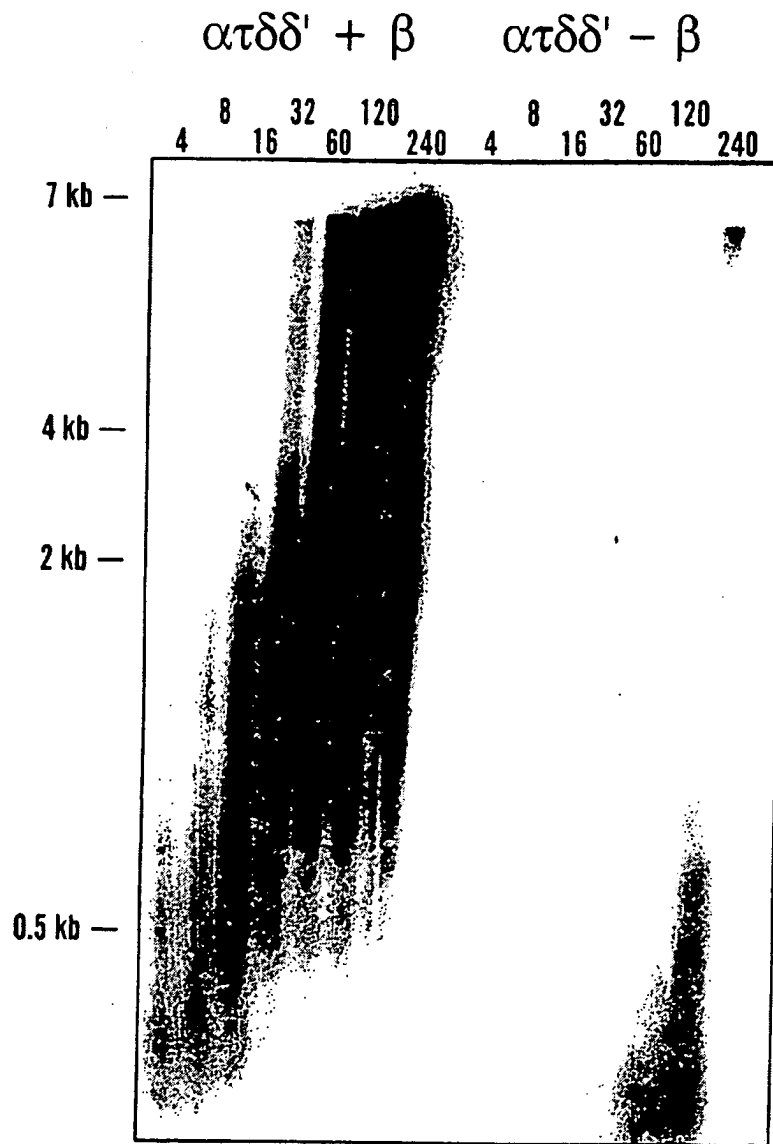


FIG. 30

REPLACEMENT
SHEET

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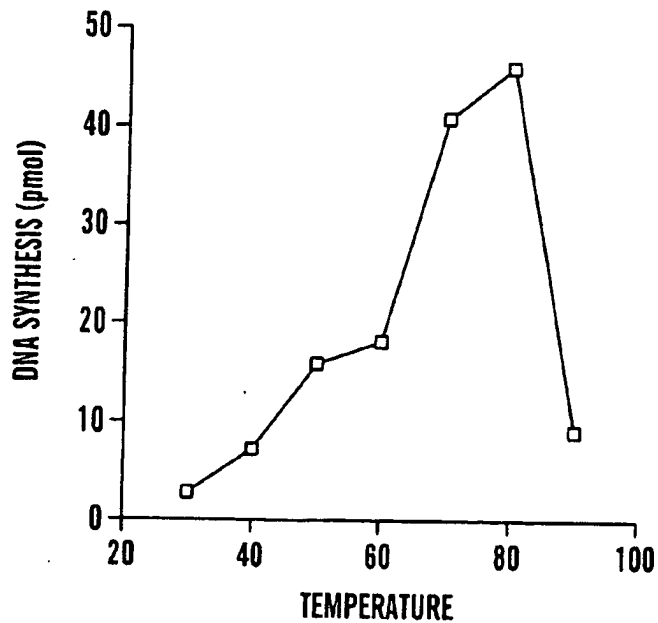


FIG. 31

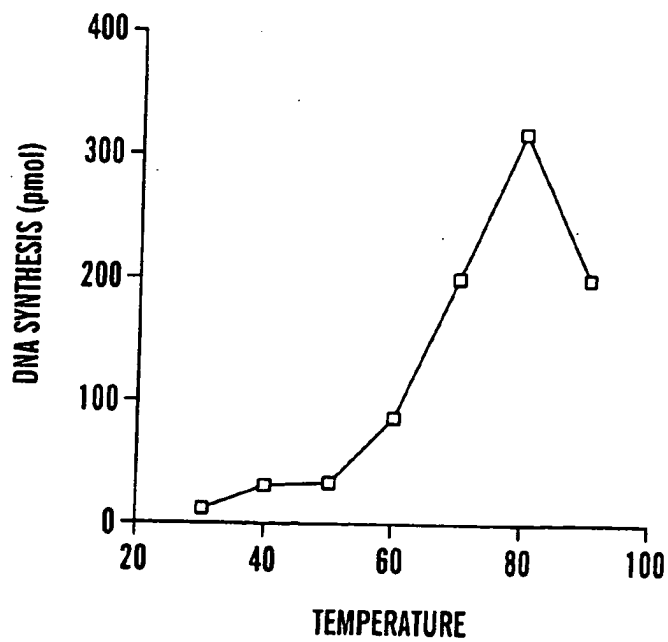


FIG. 32

REPLACEMENT SHEET

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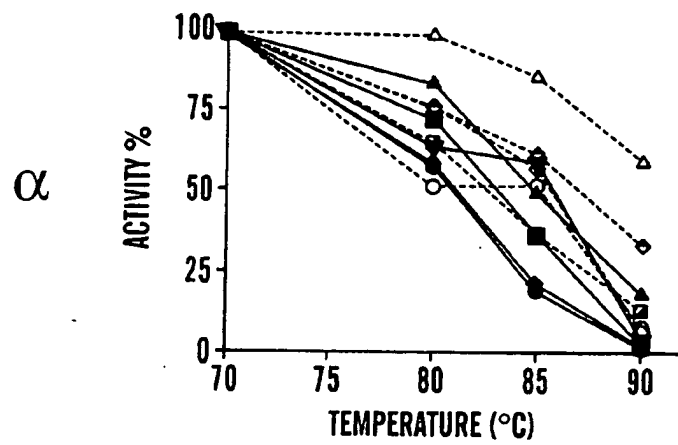


FIG. 33A

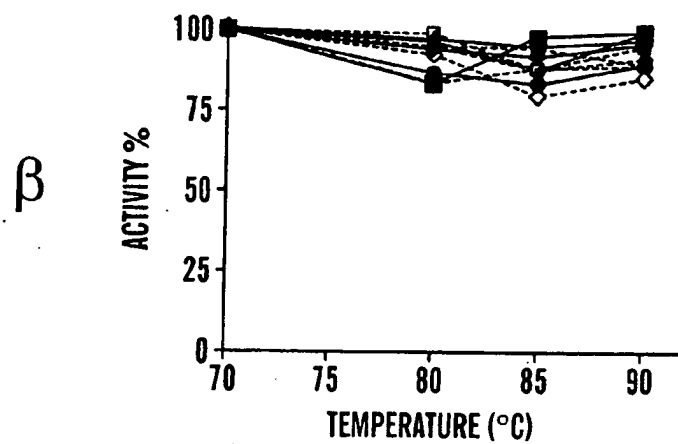


FIG. 33B

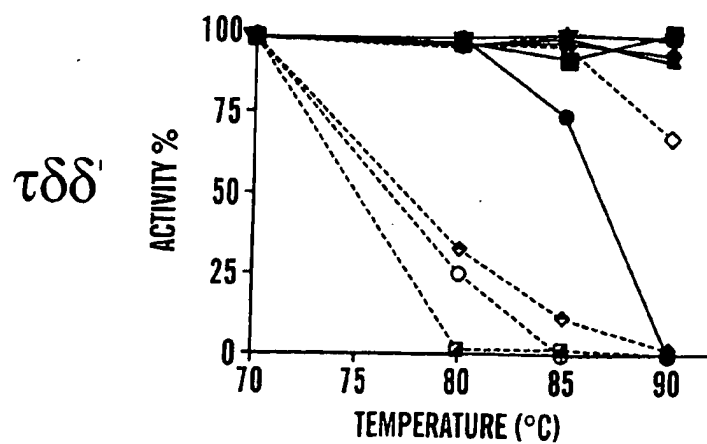


FIG. 33C

REPLACEMENT
SHEET

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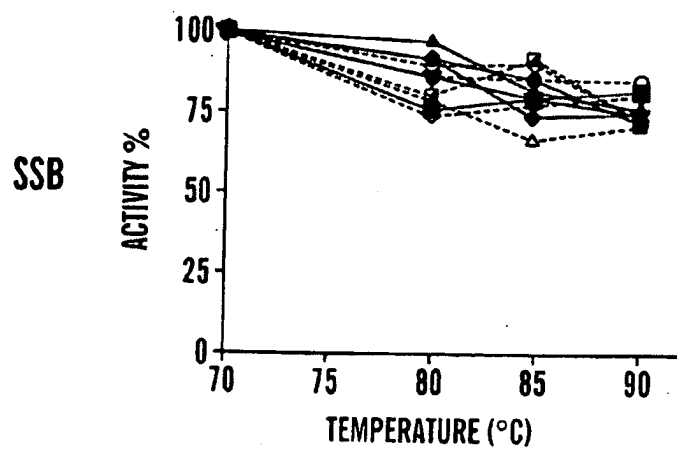


FIG. 33D

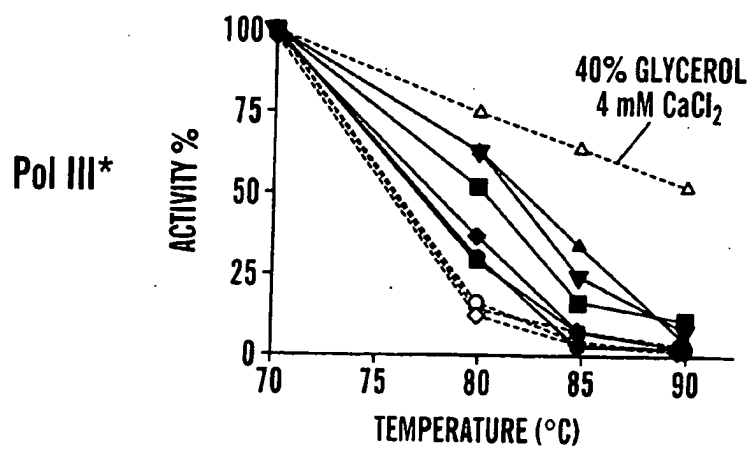


FIG. 33E

REPLACEMENT SHEET

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| | |
|--|------|
| ATGAGTAAGGATTTTCGTCCACCTTCACCTGCACACCCAGTTCTCACTCCT | |
| GGACGGGGCTATAAAGATAGACGAGCTCGTGAAAAAGGCAAAGGAGTATG | 100 |
| GATACAAAGCTGTTCGGAATGTCAGACCACGGAAACCTCTTCGGTTTCGTAT | |
| AAATTTCTACAAAGCCCTGAAGGCGGAAGGAATTAAGCCCATAATCGGCAT | 200 |
| GGAAGCCTACTTTTACCACGGGTTTCGAGGTTTGACAGAAAGACTAAAACGA | |
| GCGAGGACAACATAACCGACAAGTACAACCACCACCTCATACTTATAGCA | 300 |
| AAGGACGAAAAGGTCTAAAGAACTTAATGAAGCTCTCAACCCTCGCCTAC | |
| AAAGAAGGTTTTTTACTACAAACCCAGAATTGATTACGAACTCCTTGAAAA | 400 |
| GTACGGGGAGGGCCTAATAGCCCTTACCGCATGCCTGAAAGGTGTTCCCA | |
| CCTACTACGCTTCTATAAACGAAGTGAAAAAGGCGGAGGAATGGGTAAAG | 500 |
| AAGTTCAAGGATATATTCGGAGATGACCTTTATTTAGAACTTCAAGCGAA | |
| CAACATTTCAGAACAGGAAGTGGCAAACAGGAACTTAATAGAGATAGCCA | 600 |
| AAAAGTACGATGTGAAACTCATAGCGACGCAGGACGCCCCTACCTCAAT | |
| CCCGAAGACAGGTACGCCCACACGGTTCTTATGGCACTTCAAATGAAAAA | 700 |
| GACCATTTCACGAACTGAGTTCGGGAAACTTCAAGTGTTCAAACGAAGACC | |
| TTCACTTTTGCTCCACCCGAGTACATGTGGAAAAAGTTTGAAGGTAAAGTTC | 800 |
| GAAGGCTGGGAAAAGGCACTCCTGAACACTCTCGAGGTAATGGAAAAGAC | |
| AGCGGACAGCTTTGAGATATTTGAAAACCTCCACCTACCTCCTTCCCAAGT | 900 |
| ACGACGTTCCGCCCCGACAAAACCTTGAGGAATACCTCAGAGAATCGCG | |
| TACAAAGGTTTAAAGACAGAGGATAGAAAGGGGACAAGCTAAGGATACTAA | 1000 |
| AGAGTACTGGGAGAGGCTCGAGTACGAACTGGAAGTTATAAACAAAATGG | |
| GCTTTGCGGGATACTTCTTGATAGTTCAGGACTTCATAAACTGGGCTAAG | 1100 |
| AAAAACGACATACCTGTTGGACCCCGAAGGGGAAGTGCTGGAGGTTCCCT | |
| CGTCGCATACGCCATCGGAATAACGGACGTTGACCTTATAAAGCACGGAT | 1200 |
| TCCTTTTTTGAGAGGTTCTTAAACCCCGAAAGGGTTTCCATGCCGGATATA | |
| GACGTGGATTTCTGTTCAGGACAACAGGGAAAAGGTCATAGAGTACGTAAG | 1300 |
| GAACAAGTACGGACACGACAACGTAGCTCAGATAATCACCTACAACGTAA | |
| TGAAGGCGAAGCAAACACTGAGAGACGTCGCAAGGGCCATGGGACTCCCC | 1400 |
| TACTCCACCGCGGACAAACTCGCAAACTCATTCCTCAGGGGGACGTTCA | |
| GGGAACGTGGCTCAGTCTGGAAGAGATGTACAAAACGCCTGTGGAGGAAC | 1500 |
| TCCTTCAGAAGTACGGAGAACACAGAACGGACATAGAGGACAACGTAAAG | |
| AAGTTCAGACAGATATGCGAAGAAAGTCCGGAGATAAAACAGCTCGTTGA | 1600 |
| GACGGCCCTGAAGCTTGAAGGTCTCACGAGACACACCTCCCTCCACGCCG | |
| CGGGAGTGGTTATAGCACCAAAGCCCTTGAGCGAGCTCGTTCCCTCTAC | 1700 |
| TACGATAAAGAGGGCGAAGTCGCAACCCAGTACGACATGGTTCAGCTCGA | |
| AGAACTCGGTCTCCTGAAGATGGACTTCCTCGGACTCAAACCCCTCACAG | 1800 |
| AACTGAACTCATGAAAGAACTCATAAAGGAAAGACACGGAGTGGATATA | |
| AACTTCCTTGAACCTTCCCCTTGACGACCCGAAAGTTTACAACTCCTTCA | 1900 |
| GGAAGGAAAAACCACGGGAGTGTTCCAGCTCGAAAGCAGGGGAATGAAAG | |
| AACTCCTGAAGAACTAAAGCCCGACAGCTTTGACGACATCGTTGCGGTC | 2000 |
| CTCGCACTCTACAGACCCGGACCTCTAAAGAGCGGACTCGTTGACACATA | |
| CATTAAGAGAAAGCACGGAAAAGAACCCTTGAGTACCCCTTCCCGGAGC | 2100 |
| TTGAACCCGTCCTTAAGGAAACCTACGGAGTAATCGTTTATCAGGAACAG | |
| GTGATGAAGATGTCTCAGATACTTTCCGGCTTTACTCCCGGAGAGGCGGA | 2200 |
| TACCCTCAGAAAGGCGATAGGTAAGAAGAAAGCGGATTTAATGGCTCAGA | |
| TGAAAGACAAGTTCATACAGGGAGCGGTGGAAAGGGGATACCCTGAAGAA | 2300 |
| AAGATAAGGAAGCTCTGGGAAGACATAGAGAAGTTCGCTTCCTACTCCTT | |
| CAACAAGTCTCACTCGGTAGCTTACGGGTACATCTCCTACTGGACCGCCT | 2400 |

FIG. 34A

REPLACEMENT
SHEET

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| | |
|---|------|
| ACGTTAAAGCCCCTATCCCGCGGAGTTCTTCGCGGTAAAACTCACAAC | |
| GAAAAGAACGACAACAAGTTCCTCAACCTCATAAAAGACGCTAAACTCTT | 2500 |
| CGGATTTGAGATACTTCCCCCGACATAAACAAGAGTGATGTAGGATTTA | |
| CGATAGAAGGTGAAAACAGGATAAGGTTCTGGGCTTGCGAGGATAAAGGGA | 2600 |
| GTGGGAGAGGAACTGCTAAGATAATCGTTGAAGCTAGAAAGAAGTATAA | |
| GCAGTTCAAAGGGCTTGCGGACTTCATAAACAAAACCAAGAACAGGAAGA | 2700 |
| TAAACAAGAAAGTCGTGGAAGCACTCGTAAAGGCAGGGGCTTTTGACTTT | |
| ACTAAGAAAAAGAGGAAAGAACTACTCGCTAAAGTGGCAAACCTCTGAAAA | 2800 |
| AGCATTAATGGCTACACAAAACCTCCCTTTTCGGTGCACCGAAAGAAGAAG | |
| TGGAAGAACTCGACCCCTTAAAGCTTGAAAAGGAAGTTCTCGGTTTTTAC | 2900 |
| ATTTAGGGCAGCCCTTGACAACCTACGAAAAGCTCCTCAAGAACCGCTA | |
| CACACCCATTGAAGATTTAGAAGAGTGGGACAAGGAAAGCGAAGCGGTGC | 3000 |
| TTACAGGAGTTATCACGGAACCTCAAAGTAAAAAAGACGAAAAACGGAGAT | |
| TACATGGCGGTCTTCAACCTCGTTGACAAGACGGGACTAATAGAGTGTGT | 3100 |
| CGTCTTCCCGGGAGTTTACGAAGAGGCAAAGGAACTGATAGAAGAGGACA | |
| GAGTAGTGGTAGTCAAAGGTTTTCTGGACGAGGACCTTGAAACGGAAAAT | 3200 |
| GTCAAGTTCGTGGTGAAAGAGGTTTTCTCCCTGAGGAGTTCGCAAAGGA | |
| GATGAGGAATACCCTTTATATATTCTTAAAAAGAGAGCAAGCCCTAAACG | 3300 |
| GCGTTGCCGAAAACTAAAGGGAATTATTGAAAACAACAGGACGGAGGAC | |
| GGATACAACTTGTTCTCACGGTTGATCTGGGAGACTACTTCGTTGATTT | 3400 |
| AGCACTCCCAAGATATGAACTAAAGGCTGACAGAAAGGTTGTAGAGG | |
| AGATAGAAAACTGGGAGTGAAGGTCATAATTTAGTAAATAACCCTTACT | 3500 |
| TCCGAGTAGTCCCC | |

FIG. 34B

REPLACEMENT SHEET

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| | |
|---|------|
| MSKDFVHLHLHTQFSLLDGAIKIDELVKKAKEYGYKAVGMSDHGNLFGSY | |
| KFYKALKAEIGIKPIIGMEAYFTTGSRFDRKTKTSEDNITDKYNHHLILIA | 100 |
| KDDKGLKNLMKLSTLAYKEGFYKPRIDYELLEKYGEGLIALTACLKGVP | |
| TYYASINEVKKAEWVKKFKDIFGDDLYLELQANNIPEQEVANRNLIIEIA | 200 |
| KKYDVKLIATQDAHYLNPEDRYAHTVLMALQMKKTIHELSSGNFKCSNED | |
| LHFAPPEYMWKKFEGKFEGWEKALLNTLEVMEKTADSFEIFENSTYLLPK | 300 |
| YDVPPDKTLEEYLRELAYKGLRQRIERGQAKDTKEYWERLEYELEVINKM | |
| GFAGYFLIVQDFINWAKKNDIPVGPGRGSAGGSLVAYAIGITDVDPIKHG | 400 |
| FLFERFLNPERVSMPDIDVDFCQDNREKVIEWVRNKYGHDNVAQIITYNV | |
| MKAKQTLRDVARAMGLPYSTADKLAKLIPQGDVQGTWLSLEEMYKTPVEE | 500 |
| LLQKYGEHRDIEDNVKKFRQICEESPEIKQLVETALKLEGLTRHTSLHA | |
| AGVVIAPKPLSELVPLYDKEGEVATQYDMVQLEELGLLKMDFLGLKTLT | 600 |
| ELKLMKELIKERHGVDFINFLELPLDDPKVYKLLQEGKTTGVFQLESRGMK | |
| ELLKKLKPDSSFDDIVAVLALYRPGPLKSGLVDTYIKRKHGKEPVEYPFPE | 700 |
| LEPVLKETYGIVIVYQEQVMKMSQILSGFTPGEADTLRKAIGKKKADLMAQ | |
| MKDKFIQGAVERGYPEEKIRKLWEDIEKFASYSFNKSHSVAYGYISYWTA | 800 |
| YVKAHYPAEFFAVKLTTEKNDNKFLNLIKDAKLFGFEILPPDINKSDVGF | |
| TIEGENRIRFGLARIKGVGEETAKIIVEARKKYKQFKGLADFINKTKNRK | 900 |
| INKKVVEALVKAGAFDFTKKKRKELLAKVANSEKALMATQNSLFGAPKEE | |
| VEELDPLKLEKEVLGFYISGHPLDNYEKLKKNRYTPIEDLEEWDKESEAV | 1000 |
| LTGVITELKVKKTKNGDYMAVFNLVDKTGLIECVVFPGVYEEAKELIEED | |
| RVVVVKGFLDEEDLETVNVKFVVKEVFSPEEFAKEMRNTLYIFLKREQALN | 1100 |
| GVAEKLKGI IENNRTEDGYNLVLTVDLGDYFVDLALPQDMKLKADRKVVE | |
| EIEKLGVKVII | 1161 |

FIG. 35

REPLACEMENT SHEET

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| | |
|--|------|
| ATGAACTACGTTCCCTTCGCGAGAAAGTACAGACCGAAATTCTTCAGGGA | |
| AGTAATAGGACAGGAAGCTCCCGTAAGGATACTCAAAAACGCTATAAAAA | 100 |
| ACGACAGAGTGGCTCACGCCTACCTCTTTGCCGGACCGAGGGGGGTGGG | |
| AAGACGACTATTGCAAGAATTCTCGCAAAAGCTTTGAACTGTAAAAATCC | 200 |
| CTCCAAAGGTGAGCCCTGCGGTGAGTGCGAAAACTGCAGGGAGATAGACA | |
| GGGGTGTGTTCCCTGACTTAATTGAAATGGATGCCGCCTCAAACAGGGGT | 300 |
| ATAGACGACGTAAGGGCATTAAAAGAAGCGGTCAATTACAAACCTATAAA | |
| AGGAAAGTACAAGGTTTACATAATAGACGAAGCTCACATGCTCACGAAAG | 400 |
| AAGCTTTCAACGCTCTCTTAAAAACCCTCGAAGAGCCCCCTCCCAGAACT | |
| GTTTTCGTCCCTTGTACCACGGAGTACGACAAAAATTCTTCCCACGATACT | 500 |
| CTCAAGGTGTCAGAGGATAATCTTCTCAAAGGTAAAGAAAGGAAAAAGTAA | |
| TAGAGTATCTAAAAAGATATGTGAAAAGGAAGGGATTGAGTGCGAAGAG | 600 |
| GGAGCCCTTGAGGTTCTGGCTCATGCCTCTGAAGGGTGATGAGGGATGC | |
| AGCCTCTCTCCTGGACCAGGCGAGCGTTTACGGGGAAGGCAGGGTAACAA | 700 |
| AAGAAGTAGTGGAGAACTTCCTCGGAATTCTCAGTCAGGAAAGCGTTAGG | |
| AGTTTTCTGAAATTGCTTCTGAACTCAGAAGTGGACGAAGCTATAAAGTT | 800 |
| CCTCAGAGAACTCTCAGAAAAGGGCTACAACCTGACCAAGTTTTGGGAGA | |
| TGTTAGAAGAGGAAGTGAGAAACGCAATTTTAGTAAAGAGCCTGAAAAAT | 900 |
| CCCGAAAGCGTGGTTCAGAACTGGCAGGATTACGAAGACTTCAAAGACTA | |
| CCCTCTGGAAGCCCTCCTCTACGTTGAGAACCTGATAAACAGGGGTAAAG | 1000 |
| TTGAAGCGAGAACGAGAGAACCCCTTAAGAGCCTTTGAACTCGCGGTAAATA | |
| AAGAGCCTTATAGTCAAAGACATAATTCCCGTATCCCAGCTCGGAAGTGT | 1100 |
| GGTAAAGGAAACCAAAAAGGAAGAAAAGAAAGTTGAAGTAAAAGAAGAGC | |
| CAAAAGTAAAAGAAGAAAAACCAAAGGAGCAGGAAGAGGACAGGTTCCAG | 1200 |
| AAAGTTTTTAAACGCTGTGGACGGCAAAATCCTTAAAAGAATACTTGAAGG | |
| GGCAAAAAGGGAAGAAAGAGACGGAAAAATCGTCCTAAAGATAGAAGCCT | 1300 |
| CTTATCTGAGAACCATGAAAAAGGAATTTGACTCACTAAAGGAGACTTTT | |
| CCTTTTTTTAGAGTTTGAACCCGTGGAGGATAAAAAAACCTCAGAAGTC | 1400 |
| CAGCGGGACGAGGCTGTTTTAAAGGTAAAGGAGCTCTTCAATGCAAAAAT | |
| ACTCAAAGTACGAAGTAAAAGCTAAGGTCATAAAGGTGAGAATGCCCGTG | 1500 |
| GAAGAGATAGGGCTGTTTAACGCACTAATAGACGGCTTGCCCAGGTACGC | |
| ACTCACGAGGACGAAGGAAAAGGGAAAGGGAGAAGTTTTTCGTTTTAGCGA | 1600 |
| CTCCTTATAAAGTCAAGGAATTGATGGAAGCTATGGAGGGTATGAAAAAA | |
| CACATAAAGGATTTAGAAATCCTCGGAGAGACGGATGAGGATTTAACTTT | 1700 |
| TTAAAGTATGGGTGTATCTGAGCAAAGGTTTAAGCTAAAAACAAACCTGA | |
| AACCCGCAGGGGACCAGCCGAAAGCCATAAAAAAACTCCTTGAAAACCTA | 1800 |
| AGGAAAGGCGTAAAAGAACAACACTTCTCGGAGTCACGGGAAGCGGAAA | |
| GACTTTTACTCTAGCAAACGTAATAGCGAAGTACAACAAACCAACTCTTG | 1900 |
| TGGTAGTTTACAACAAAATTCTCGCGGCACAGCTATACAGGGAGTTTAAA | |
| GAACTATTCCCTGAAAACGCTGTAGAGTACTTTGTCTCTTACTACGACTA | 2000 |
| TTACCAACCTGAAGCCTACATTCCCGAAAAAGATTTATACATAGAAAAGG | |
| ACGCGAGTATAAACGAAAGCTGGAACGTTTCAGACACTCCGCCACGATAT | 2100 |
| CCGTTCTAGAAAGGAGGGACGTTATAGTAGTTGCTTCAGTTTCTTGCATA | |
| TACGGACTCGGGAAACCTGAGCACTACGAAAACCTGAGGATAAACTCCA | 2200 |
| AAGGGGAATAAGACTGAACTTGAGTAAGCTCCTGAGGAACTCGTTGAGC | |
| TAGGATATCAGAGAAATGACTTTGCCATAAAGAGGGCTACCTTCTCGGTT | 2300 |
| AGGGGAGACGTGGTTGAGATAGTCCCTTCTCACACGGAAGATTACCTCGT | |
| GAGGGTAGAGTTCTGGGACGACGAAGTTGAAAGAATAGTCCTCATGGACG | 2400 |
| CTCTGAAC | |

FIG. 36

REPLACEMENT
SHEET

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| | |
|---|-----|
| MNYVPFARKYRPKFFREVIGQEAPVRILKNAIKNDRVAHAYLFAGPRGVG | |
| KTTIARILAKALNCKNPSKGEPCGECENCREIDRGVFPDLIEMDAASNRG | 100 |
| IDDVRLKEAVNYKPIKGKYKVYIIDEAHMLTKEAFNALLKTLEPPPPRT | |
| VFVLCCTTEYDKILPTILSRCQRIIFSKVRKEKVIEYLKKICEKEGIECEE | 200 |
| GALEVLAHASEGCMRDAASLLDQASVYGEGRVTKEVVENFLGILSQESVR | |
| SFLKLLLNSEVDEAIKFLRELSEKGYNLTKFWEMLEEEVRNAILVKSLKN | 300 |
| PESVVQNWQDYEDFKDYPLEALLYVENLINRGKVEARTREPLRAFELAVI | |
| KSLIVKDIIPVSQLGSSVKETKKEEKKEVKEEPKVKEEKPKQEEDRFQ | 400 |
| KVLNAVDGKILKRILEGAKREERDGGKIVLKIEASYLRTMKKEFDSLKETF | |
| PFLEFEPVEDKKKPQKSSGTRLF | 473 |

FIG. 37

REPLACEMENT SHEET

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| | |
|---|------|
| ATGCGCGTTAAGGTGGACAGGGAGGAGCTTGAAGAGGTTCTTAAAAAAGC | |
| AAGAGAAAGCACGGAAAAAAGCCGCACTCCCGATACTCGCGAACTTCT | 100 |
| TACTCTCCGCAAAAGAGGAAAACTTAATCGTAAGGGCAACGGACTTGGA | |
| AACTACCTTGTAAGTCTCCGTAAAGGGGGAGGTTGAAGAGGAAGGAGAGGT | 200 |
| TTGCGTCCACTCTCAAAAACTCTACGATATAGTCAAGAACTTAAATTCGG | |
| CTTACGTTTACCTTCATACGGAAGGTGAAAACTCGTCATAACGGGAGGA | 300 |
| AAGAGTACGTACAACTTCCGACAGCTCCCGCGGAGGACTTTCCCGAATT | |
| TCCAGAAATCGTAGAAGGAGGAGAAACACTTTCGGGAAACCTTCTCGTTA | 400 |
| ACGGAATAGAAAAGGTAGAGTACGCCATAGCGAAGGAAGAAGCGAACATA | |
| GCCCTTCAGGGAATGTATCTGAGAGGATACGAGGACAGAATTCACTTTGT | 500 |
| GTTTCGGACGGTCACAGGCTTGCACTTTATGAACCTCTACGTAAACATTGA | |
| AAAGAGTGAAGACGAGTCTTTTGCTTACTTCTCCACTCCCGAGTGGAAC | 600 |
| TCGCCGTTAGCTCCTGGAAGGAGAATTCCCGGACTACATGAGTGTCATCC | |
| CTGAGGAGTTTTTCGGCGGAAGTCTTGTTTGAGACAGAGGAAGTCTTAAAG | 700 |
| GTTTTAAAGAGGTTGAAGGCTTTAAGCGAAGGAAAAGTTTTTCCCGTGAA | |
| GATTACCTTAAGCGAAAACCTTGCCATCTTTGAGTTCGCGGATCCGGAGT | 800 |
| TCGGAGAAGCGAGAGAGGAAATTGAAGTGGAGTACACGGGAGAGCCCTTT | |
| GAGATAGGATTCAACGGAAATACCTTATGGAGGCGCTTGACGCCTACGAC | 900 |
| AGCGAAAGAGTGTGGTTCAAGTTCACAACCCCCGACACGGCCACTTTATT | |
| GGAGGCTGAAGATTACGAAAAGGAACCTTACAAGTGCATAATAATGCCGA | 1000 |
| TGAGGGTGTAGCCATGAAAAAGCTTTAATCTTTTTATTGAGCTTGAGCC | |
| TTTTAATTCCTGCGTTTAGCGAAGCCAAACCCAAGTCTTC | 1090 |

FIG. 38

| | |
|--|-----|
| MRVKVDREELEEVLLKKARESTEKKAALPILANFLLSAKEENLIVRATDLE | |
| NYLVVSVKGEVEEEGEVVCVHSQKLYDIVKNLNSAYVYLHTEGEKLVITGG | 100 |
| KSTYKLPAPAEDEFPEFPEIVEGGETLSGNLLVNGIEKVEYAIKKEEANI | |
| ALQGMYLRGYEDRIHFVGS DGHRLALYEPLGEFSKELLI PRKSLKVLKKL | 200 |
| ITGIEDVNI EKSEDES FAYFSTPEWKLAVRLLEGEFPDYMSVIPEEFSAE | |
| VLFPETEEVLKVLKRLKALSEGKVFPVKITLSENLAIFE FADPEFGEAREE | 300 |
| IEVEYTGEPFEIGFNGKYLMEALDAYDSERVWFKFTTPDTATLLEAEDYE | |
| KEPYKCIIMPMRV | 363 |

FIG. 39

REPLACEMENT SHEET

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GTGGAAACCACAATATTCCAGTTCCAGAAAACCTTTTTTCACAAAACCTCC
GAAGGAGAGGGTCTTCGTCCTTCATGGAGAAGAGCAGTATCTCATAAGAA 100
CCTTTTTGTCTAAGCTGAAGGAAAAGTACGGGGAGAATTACACGGTTCTG
TGGGGGGATGAGATAAGCGAGGAGGAATTCTACACTGCCCTTTCCGAGAC 200
CAGTATATTTCGGCGGTTCAAAGGAAAAAGCGGTGGTCATTTACAACCTTCG
GGGATTTTCCTGAAGAAGCTCGGAAGGAAGAAAAAGGAAAAAGAAAGGCTT 300
ATAAAAGTCCTCAGAAACGTAAAGAGTAACTACGTATTTATAGTGATCGA
TGCGAAACTCCAGAAACAGGAACTTTCTTCGGAACCTCTGAAATCCGTAG 400
CGTCTTTTCGGCGGTATAGTGGTAGCAAACAGGCTGAGCAAGGAGAGGATA
AAACAGCTCGTCCTTAAGAAGTTCAAAGAAAAAGGGATAAACGTAGAAAA 500
CGATGCCCTTGAATACCTTCTCCAGCTCACGGGTTACAACCTTGATGGAGC
TCAAACCTTGAGGTTGAAAAACTGATAGATTACGCAAGTGAAAAGAAAATT 600
TTAACACTCGATGAGGTAAAGAGAGTAGCCTTCTCAGTCTCAGAAAACGT
AAACGTATTTGAGTTCGTTGATTTACTCCTCTTAAAAGATTACGAAAAGG 700
CTCTTAAAGTTTTGGACTCCCTCATTTCTTCGGAATACACCCCTCCAG
ATTATGAAAATCCTGTCCTCCTATGCTCTAAAACCTTACACCCTCAAGAG 800
GCTTGAAGAGAAGGGAGAGGACCTGAATAAGGCGATGGAAAGCGTGCGGAA
TAAAGAACAACCTTTCTCAAGATGAAGTTCAAATCTTACTTAAAGGCAAAC 900
TCTAAAGAGGACTTGAAGAACCTAATCCTCTCCCTCCAGAGGATAGACGC
TTTTTCTAACTTTACTTTTCAGGACACAGTGCAGTTGCTGGGGATTTCTT 1000
GACCTCAAGACTGGAGAGGGAAGTTGTGAAAAATACTTCTCATGGTGGAT
AATCTTTTTTATGAAGTTTGCAGTTTTCGTTTTCCTCCGTTCT 1093

FIG. 40

VETTIFQFQKTFFTKPPKERVFLHGEEQYLIRTFLSKLKEYGENYTVL
WGDEISEEEFYTALSETSIFGGSKEKAVVIYNFGDFLKKLGRKKKEKERL 100
IKVLRNVKSNYVFIVYDAKLQKQELSSEPLKSVASFGGIVVANRLSKERI
KQLVLKKFKEKGINVENDALEYLLQLTGYNLMELKLEVEKLIDYASEKKI 200
LTLDEVKRVAFSVSENVNVEFVDLLLLLDYKALKVLDLSLISFGIHPLO
IMKILSSYALKLYTLKRLEEKGEDLNKAMESVGIKNNFLKMKFKSYLKAN 300
SKEDLKNLILSLQRIDAFSKLYFQDTVQLLRDFLTSRLEREVVKNTSHGG

FIG. 41

REPLACEMENT SHEET

55/83

| | |
|--|------|
| ATGGAAAAAGTTTTTTTGGAAAACTCCAGAAAACCTTGCACATACCCGG | |
| AGGACTCCTTTTTTTTACGGCAAAGAAGGAAGCGGAAAGACGAAAACAGCTT | 100 |
| TTGAATTTGCAAAAGGTATTTTTATGTAAGGAAAACGTACCTGGGGATGCG | |
| GAAGTTGTCCCTCCTGCAAACACGTAAACGAGCTGGAGGAAGCCTTCTTT | 200 |
| AAAGGAGAAATAGAA'GACTTTAAAGTTTATAAGACAAGGACGGTAAAAAG | |
| CACTTCGTTTACCTTATGGGCGAACATCCCGACTTTGTGGTAATAATCCC | 300 |
| GAGCGGACATTACATAAAGATAGAACAGATAAGGGAAGTTAAGAAGTTTG | |
| CCTATGTGAAGCCCCGCACTAAGCAGGAGAAAAAGTAATTATAATAGACGAC | 400 |
| GCCCACGCGATGACCTCTCAGGCGGCAAACGCTCTTTTAAAGGTATTGGA | |
| AGAGCCACCTGCGGACACCACCTTTATCTTGACCACGAACAGGCGTTCTG | 500 |
| CAATCCTGCCGACTATCCTCTCCAGAAGTTTCAAGTGGAGTTCAAGGGC | |
| TTTTCAGTAAAAGAGGTTATGGAAATAGCGAAAGTAGACGAGGAAATAGC | 600 |
| GAAACTCTCTGGAGGCAGTCTAAAAAGGGCTATCTTACTAAAGGAAAACA | |
| AAGATATCCTAAACAAAGTAAAGGAATTCTTGGAACGAGCCGTAAAA | 700 |
| GTTTACAAGCTTGCAAGTGAATTTCGAAAAGTGGGAACCTGAAAAGCAAAA | |
| ACTCTTCCTTGAAATTATGGAAGAATTGGTATCTCAAAAATTGACCGAAG | 800 |
| AGAAAAAAGACAATTACACCTACCTTCTTGATACGATCAGACTCTTTAAA | |
| GACGGACTCGCAAGGGGTGTAAACGAACCTCTGTGGCTGTTTACGTTAGC | 900 |
| CGTTCAGGCGGATTAATAAACCGTTATTGATTCCGTAACATTTAAACCTT | |
| AATCTAAATTATGAGAGCCTTTGAAGGAGGTCTGGTATGGAAAATTTGAA | 1000 |
| GATTAGATATATAGATACGAGGAAGATAGGAACCGTGAGCGGTGTAAAAG | |
| T | 1051 |

FIG. 42

| | |
|--|-----|
| MEKVFLEKLQKTLHIPGGLLFYKGESGKTKTAFEFAGILCKENVPWGC | |
| GSCPSCKHVNELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVII | 100 |
| PSGHYIKIEQIREVKNFAYVKPALSRRKVIIIDDAHAMTSQAANALLKVL | |
| EEPPADTTFILTTNRRSAILPTILSRTFQVEFKGFSVKEVMEIAKVDEEI | 200 |
| AKLSGGSLKRAILLKENKDILNKVKEFLNEPLKVYKLASEFEKWEPEKQ | |
| KLFLEIMEELVSQKLTEEKKNYTYLLDTIRLFKDG LARGVNEPLWLFTL | 300 |
| AVQAD | |

FIG. 43

REPLACEMENT
SHEET

56/83

| | |
|--|-----|
| ATGAACTTCCTGAAAAAGTTCCTTTTACTGAGAAAAGCTCAAAAGTCTCC | |
| TTACTTCGAAGAGTTCTACGAAGAAATCGATTTGAACCAGAAGGTGAAAG | 100 |
| ATGCAAGGTTTGTAGTTTTTGACTGCGAAGCCACAGAACTCGACGTAAAG | |
| AAGGCAAAACTCCTTTCAATAGGTGCGGTTGAGGTTAAAAACCTGGAAAT | 200 |
| AGACCTCTCTAAATCTTTTTACGAGATACTCAAAAGTGACGAGATAAAGG | |
| CGGCGGAGATACATGGAATAACCAGGGAAGACGTTGAAAAGTACGGAAAG | 300 |
| GAACCAAAGGAAGTAATATACGACTTTCTGAAGTACATAAAGGGAAGCGT | |
| TCTCGTTGGCTACTACGTGAAGTTTGACGTCTCACTCGTTGAGAAGTACT | 400 |
| CCATAAAGTACTTCCAGTATCCAATCATCAACTACAAGTTAGACCTGTTT | |
| AGTTTCGTGAAGAGAGAGTACCAGAGTGGCAGGAGTCTTGACGACCTTAT | 500 |
| GAAGGAACTCGGTGTAGAAATAAGGGCAAGGCACAACGCCCTTGAAGATG | |
| CCTACATAACCGCTCTTCTTTTCCTAAAGTACGTTTACCCGAACAGGGAG | 600 |
| TACAGACTAAAGGATCTCCCGATTTTCCTT | |

FIG. 44

| | |
|---|-----|
| MNFLKKFLLLRKAQKSPYFEEFYEEIDLNQVKVDARFVVFDCATELDVK | |
| KAKLLSIGAVEVKNLEIDLKSKSFYEILKSDEIKAAEIHGITREDVEKYGK | 100 |
| EPKEVIYDFLKYIKGSLVGVYVKFDVSLVEKYSIKYFQYPIINYKLDLF | |
| SFVKREYQSGRSLDDLMKELGVEIRARHNALEDAYITALLFLKYVYPNRE | 200 |
| YRLKDLPIFL | |

FIG. 45

REPLACEMENT
SHEET

57/83

| | |
|---|-----|
| ATGCTCAATAAGGTTTTTATAATAGGAAGACTTACGGGTGACCCCGTTAT | |
| AACTTATCTACCGAGCGGAACGCCCGTAGTAGAGTTTACTCTGGCTTACA | 100 |
| ACAGAAGGTATAAAAACCAGAACGGTGAATTTTCAGGAGGAAAGTCACTTC | |
| TTTGACGTAAAGGCGTACGGAAAAATGGCTGAAGACTGGGCTACACGCTT | 200 |
| CTCGAAAGGATACCTCGTACTCGTAGAGGGAAGACTCTCCAGGAAAAGT | |
| GGGAGAAAGAAGGAAAGAAGTTCTCAAAGGTCAGGATAATAGCGGAAAAC | 300 |
| GTAAGATTAATAAACAGGCCGAAAGGTGCTGAACTTCAAGCAGAAGAAGA | |
| GGAGGAAGTTCCTCCCATTGAGGAGGAAATTGAAAACTCGGTAAAGAGG | 400 |
| AAGAGAAGCCTTTTACCGATGAAGAGGACGAAATACCTTTTAAATTTTGA | |
| GGAGGTTAAAGTATGGTAGTGAGAGCTCCTAAGAAGAAAGTTTGTATGTA | 500 |
| CTGTGAACAAAAGAGAGAGCCAGATT | |

FIG. 46

| | |
|--|-----|
| MLNKVFIIGRLTGDPVITYLPSGTPVVEFTLAYNRRYKNQNGEFQEESHF | |
| FDVKAYGKMAEDWATRFSGYLVLVEGRLSQEKWEKEGKKFSKVRIIAEN | 100 |
| VRLINRPKGAELOAEEEEVPPIEEEIEKLGKEEEKPFTDEEDEIPF | |

FIG. 47

REPLACEMENT SHEET

58/83

| | |
|---|------|
| ATGCAATTTGTGGATAAACTTCCCTGTGACGAATCCGCCGAGAGGGCGGT | |
| TCTTGGCAGTATGCTTGAAGACCCCGAAAACATACCTCTGGTACTTGAAT | 100 |
| ACCTTAAAGAAGAAGACTTCTGCATAGACGAGCACAAGCTACTTTTCAGG | |
| GTTCTTACAAACCTCTGGTCCGAGTACGGCAATAAGCTCGATTTCGTATT | 200 |
| AATAAAGGATCACCTTGAAAAGAAAACTTACTCCAGAAAATACCTATAG | |
| ACTGGCTCGAAGAACTCTACGAGGAGGCGGTATCCCCTGACACGCTTGAG | 300 |
| GAAGTCTGCAAAATAGTAAAACAACGTTCCGCACAGAGGGCGATAATTCA | |
| ACTCGGTATAGAACTCATTACAAAAGGAAAGGAAAAACAAAGACTTTTACA | 400 |
| CATTAATCGAGGAAGCCCAGAGCAGGATATTTTCCATAGCGGAAAGTGCT | |
| ACATCTACGCAGTTTTTACCATGTGAAAGACGTTGCGGAAGAAGTTATAGA | 500 |
| ACTCATTTATAAATTCAAAGCTCTGACAGGCTAGTCACGGGACTCCCAA | |
| GCGGTTTCACGGAACCTCGATCTAAAGACGACGGGATTCCACCCTGGAGAC | 600 |
| TAAATAATACTCGCCGCAAGACCCGGTATGGGGAAAACCGCCTTTATGCT | |
| CTCCATAATCTACAATCTCGCAAAGACGAGGGAAAACCCCTCAGCTGTAT | 700 |
| TTTCCTTGGAATGAGCAAGGAACAGCTCGTTATGAGACTCCTCTCTATG | |
| ATGTCGGAGGTCCCACCTTTTCAAGATAAGGTCTGGAAGTATATCGAATGA | 800 |
| AGATTTAAAGAAGCTTGAAGCAAGCGCAATAGAACTCGCAAAGTACGACA | |
| TATACCTCGACGACACACCCGCTCTCACTACAACGGATTTAAGGATAAGG | 900 |
| GCAAGAAAGCTCAGAAAGGAAAAGGAAGTTGAGTTTCGTGGCGGTGGACTA | |
| CTTGCAACTTCTGAGACCGCCAGTCCGAAAGAGTTCAAGACAGGAGGAAG | 1000 |
| TGGCAGAGGTTTCAAGAACTTAAAAGCCCTTGCAAAGGAACTTCACATT | |
| CCCGTTATGGCACTTGCGCAGCTCTCCCGTGAGGTGGAAAAGAGGAGTGA | 1100 |
| TAAAAGACCCAGCTTGCGGACCTCAGAGAATCCGGACAGATAGAACAGG | |
| ACGCAGACCTAATCCTTTTCTCCACAGACCCGAGTACTACAAGAAAAAG | 1200 |
| CCAAATCCCGAAGAGCAGGGTATAGCGGAAGTGATAATAGCCAAGCAAAG | |
| GCAAGGACCCACGGACATTGTGAAGCTCGCATTTTATTAAGGAGTACACTA | 1300 |
| AGTTTGCAAACCTAGAAGCCCTTCTGAACAACCTCCTGAAGAAGAGGAA | |
| CTTTCCGAAATTATTGAAACACAGGAGGATGAAGGATTCTGAAGATATTGA | 1400 |
| CTTCTGAAAATTAAGGTTTATAATTTTATCTTGCTATCCGGGGTAGCT | |
| CAATCGGCAGAGCGGGTGGCTG | 1472 |

FIG. 48

| | |
|---|-----|
| MQFVDKLPCEDESAERAUAVLGSMLDPENIPLVLEYLKEEDFCIDEHKLFR | |
| VLTNLWSEYGNKLDVFLIKDHLEKKNLLQKIPIDWLEELYEEAVSPDTLE | 100 |
| EVCKIVKQRSAQRAIIQLGITSTQFYHVKDVAEEVIELIYKFKSSDRLVT | |
| GLPSGFTELDLKTTFGPHGDLIIAARPGMGKTAFMLSIIYNLAKDEGKP | 200 |
| SAVFSLEMSKEQLVMRLLSMMSEVPLFKIRSGSISNEDLKKLEASAIELA | |
| KYDIYLDTPALTTTDLRIRARKLRKEKEVEFVAVDYLQLLRPPVRKSSR | 300 |
| QEEVAEVSRLKALAKELHIPVMALAQLSREVEKRSDKRPQLADLRESGQ | |
| IEQDADLILFLHRPEYYKKKPNPEEQGIAEVIIAKQRQGPTDIVKLAFIK | 400 |
| EYTKFANLEALPEQPPEEEELSEIIETQEDEGFEDIDF | |

FIG. 49

REPLACEMENT SHEET

59/83

| | |
|--|------|
| ATGTCCTCGGACATAGACGAACTTAGACGGGAAATAGATATAGTAGACGT | |
| CATTTCCGAATACTTAACTTAGAGAAGGTAGGTTCCAATTACAGAACGA | 100 |
| ACTGTCCCTTTTACCCTGACGATACACCCTCCTTTTACGTGTCTCCAAGT | |
| AAACAAATATTCAAGTGTTTCGGTTGCGGGGTAGGGGGAGACGCGATAAA | 200 |
| GTTTCGTTTCCCTTTTACGAGGACATCTCCTATTTTGAAGCCGCCCTTGAAC | |
| TCGCAAAACGCTACGGAAAGAAATTAGACCTTGAAAAGATATCAAAAGAC | 300 |
| GAAAAGGTATACGTGGCTCTTGACAGGGTTTGTGATTTCTACAGGGAAAG | |
| CCTTCTCAAAAACAGAGAGGCAAGTGAGTACGTAAAGAGTAGGGGAATAG | 400 |
| ACCCTAAAGTAGCGAGGAAGTTTGATCTTGGGTACGCACCTTCCAGTGAA | |
| GCACTCGTAAAAGTCTTAAAAGAGAACGATCTTTTAGAGGCTTACCTTGA | 500 |
| AACTAAAAACCTCCTTTCTCCTACGAAGGGTGTTTACAGGGATCTCTTTC | |
| TTCGGCGTGTCGTGATCCCGATAAAGGATCCGAGGGGAAGAGTTATAGGT | 600 |
| TTCGGTGGAAGGAGGATAGTAGAGGACAAATCTCCCAAGTACATAAACTC | |
| TCCAGACAGCAGGGTATTTAAAAGGGGGGAGAACTTATTCGGTCTTTACG | 700 |
| AGGCAAAGGAGTATATAAAGGAAGAAGGATTTGCGATACTTGTGGAAGGG | |
| TACTTTGACCTTTTGAGACTTTTTTCCGAGGGAATAAGGAACGTTGTTGC | 800 |
| ACCCCTCGGTACAGCCCTGACCCAAAATCAGGCAAACCTCCTTTCCAAGT | |
| TCACAAAAAAGGTCTACATCCTTTACGACGGAGATGATGCGGGAAGAAAG | 900 |
| GCTATGAAAAGTGCCATTCCCCTACTCCTCAGTGCAGGAGTGGAAGTTTA | |
| TCCCGTTTACCTCCCCGAAGGATACGATCCCGACGAGTTTATAAAGGAAT | 1000 |
| TCGGGAAAGAGGAATTAAGAAGACTGATAAACAGCTCAGGGGAGCTCTTT | |
| GAAACGCTCATAAAAACCGCAAGGGAAAACCTTAGAGGAGAAAACGCGTGA | 1100 |
| GTTTCAGGTATTATCTGGGCTTTATTTCCGATGGAGTAAGGCGCTTTGCTC | |
| TGGCTTCGGAGTTTTCACACCAAGTACAAAGTTCCTATGGAAATTTTATTA | 1200 |
| ATGAAAATTGAAAAAAATTCTCAAGAAAAAGAAATTAACTCTCCTTTTAA | |
| GGAAAAAATCTTCCTGAAAGGACTGATAGAATTAAAACCAAAAATAGACC | 1300 |
| TTGAAGTCCTGAACTTAAGTCCTGAGTTAAAGGAACTCGCAGTTAACGCC | |
| TTAAACGGAGAGGAGCATTTACTTCCAAAAGAAGTTCTCGAGTACCAGGT | 1400 |
| GGATAACTTGGAGAACTTTTTTAACAACATCCTTAGGGATTTACAAAAAT | |
| CTGGGAAAAAGAGGAAGAAAAGAGGGTTGAAAAATGTAAATACTTAATTA | 1500 |
| ACTTTAATAAATTTTGTAGAGTTAGGA | |

FIG. 50

| | |
|--|-----|
| MSSDIDELRREIDIVDVISEYLNLEKVGSNYRTNCPFHPDDTPSFYVSPS | |
| KQIFKCFGCGVGDAIKFVSLYEDISYFEAALELAKRYGKKLDLEKISKD | 100 |
| EKVYVALDRVCDFYRESLLKNREASEYVKSRIIDPKVARKFDLGYAPSSE | |
| ALVKVLKENDLLEAYLETKNLLSPTKGVYRDLFLRRVVIPIKDPRGRVIG | 200 |
| FGGRRIVEDKSPKYINSPDSRVFKKGENLFGLYEKEYIKEEGFAILVEG | |
| YFDLLRLFSEGIRNVVAPLGTALTQONQANLLSKFTKKVYILYDGD DAGRK | 300 |
| AMKSAIPLLLSAGVEVYPVYLPEGYDPDEFIKEFGKEELRRLINSSGELF | |
| ETLIKTARENLEEKTRFRYVLGFISDGVRRFALASEFHTKYKVPMEILL | 400 |
| MKIEKNSQEKEIKLSFKEKIFLKGLIELPKPIDLEVLNLSPELKE LAVNA | |
| LNGEEHLLPKEVLEYQVDNLEKLFNNILRDLQKSGKKRKKRGLKVNNT | 498 |

FIG. 51

REPLACEMENT
SHEET

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| | |
|---|-----|
| ATGCAAGATACCGCTACCTGCAGTATTTGTCAGGGGACGGGATTCGTAAA | |
| GACCGAAGACAACAAGGTAAGGCTCTGCGAATGCAGGTTCAAGAAAAGGG | 100 |
| ATGTAAACAGGGAACTAAACATCCCAAAGAGGTACTGGAACGCCAACTTA | |
| GACACTTACCACCCCAAGAACGTATCCCAAGAACAGGGCACTTTTGACGAT | 200 |
| AAGGGTCTTCGTCCACAACCTTCAATCCCGAGGAAGGGAAAGGGCTTACCT | |
| TTGTAGGATCTCCTGGAGTCGGCAAACTCACCTTGCGGTTGCAACATTA | 300 |
| AAAGCGATTTATGAGAAGAAGGGAATCAGAGGATACTTCTTCGATACGAA | |
| GGATCTAATATTCAGGTTAAAACACTTAATGGACGAGGGAAAGGATACAA | 400 |
| AGTTTTTAAAACTGTCTTAAACTACCGGTTTTGGTTCTCGACGACCTC | |
| GGTTCTGAGAGGCTCAGTGACTGGCAGAGGGAATCATCTCTTACATAAT | 500 |
| CACTTACAGGTATAACAACCTTAAGAGCACGATAATAACCACGAATTACT | |
| CACTCCAGAGGGAAGAAGAGAGTAGCGTGAGGATAAGTGCGGATCTTGCA | 600 |
| AGCAGACTCGGAGAAAACGTAGTTTCAAAAATTTACGAGATGAACGAGTT | |
| GCTCGTTATAAAGGGTTCCGACCTCAGGAAGTCTAAAAAGCTATCAACCC | 700 |
| CATCT | |

FIG. 52

| | |
|---|-----|
| MQDTATCSICQGTGFVKTEDNKKVRLCECRFKKRDVNRELNIPKRYWNANL | |
| DTYHPKNVSQNRALLTIRVFVHNFNPEEGKGLTFVGSPGVGKTHLAVATL | 100 |
| KAIYEKKGIRGYFFDTKDILIFRLKHLMDGKDTKFLKTVLNSPVLVLDL | |
| GSERLSDWQRELISYIITYRYNNLKSTIITNYSLQREEESSVRISADLA | 200 |
| SRLGENVVSKIYEMNELLVIKGSDLRKS KKLSTPS | |

FIG. 53

REPLACEMENT SHEET

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| | |
|--|------|
| ATGAAAAAGATTGAAAATTTGAAGTGGAAAAATGTCTCGTTTAAAAGCCT | |
| GGAAATAGATCCCGATGCAGGTGTGGTTCTCGTTTCCGTGGAAAAATTCT | 100 |
| CCGAAGAGATAGAAGACCTTGTGCGTTTACTGGAGAAGAAGACGCGGTTT | |
| CGAGTCATCGTGAACGGTGTTCAAAAAGTAACGGGGATCTAAGGGGAAA | 200 |
| GATACTTTCCCTTCTCAACGGTAATGTGCCTTACATAAAAGATGTTGTTT | |
| TCGAAGGAAACAGGCTGATTCTGAAAGTGCTTGGAGATTTCGCGCGGGAC | 300 |
| AGGATCGCCTCCAAACTCAGAAGCACGAAAAACAGCTCGATGAACTGCT | |
| GCCTCCCGGAACAGAGATCATGCTGGAGGTTGTGGAGCCTCCGGAAGATC | 400 |
| TTTTGAAAAAGGAAGTACCACAACCAGAAAAGAGAGAAGAACCAAAGGGT | |
| GAAGAATTGAAGATCGAGGATGAAAACCACATCTTTGGACAGAAACCCAG | 500 |
| AAAGATCGTCTTCACCCCTCAAAAATCTTTGAGTACAACAAAAGACAT | |
| CGGTGAAGGGCAAGATCTTCAAAATAGAGAAGATCGAGGGGAAAAGAACG | 600 |
| GTCCTTCTGATTTACCTGACAGACGGAGAAGATTCTCTGATCTGCAAAGT | |
| CTTCAACGACGTTGAAAAGGTCTGAAGGGGAAAGTATCGGTGGGAGACGTGA | 700 |
| TCGTTGCCACAGGAGACCTCCTTCTCGAAAACGGGGAGCCCACCCTTTAC | |
| GTGAAGGGAATCACAAAACCTCCCGAAGCGAAAAGGATGGACAAATCTCC | 800 |
| GGTTAAGAGGGTGGAGCTCCACGCCCATACCAAGTTCAGCGATCAGGACG | |
| CAATAACAGATGTGAACGAATATGTGAAACGAGCCAAGGAATGGGGCTTT | 900 |
| CCCGCGATAGCCCTCACGGATCATGGGAACGTTTCAGGCCATACCTTACTT | |
| CTACGACGCGGCGAAAGAAGCTGGAATAAAGCCCATTTTCGGTATCGAAG | 1000 |
| CGTATCTGGTGAGTGACGTGGAGCCCGTCATAAGGAATCTCTCCGACGAT | |
| TCGACGTTTGGAGATGCCACGTTTCGTCGTCTCGACTTCGAGACGACGGG | 1100 |
| TCTCGACCCGCGAGGTGGATGAGATCATCGAGATAGGAGCGGTGAAGATAC | |
| AGGGTGGCCAGATAGTGGACGAGTACCACACTCTCATAAAGCCTTCCAGG | 1200 |
| GAGATCTCAAGAAAAAGTTTCGGAGATCACCGGAATCACTCAAGAGATGCT | |
| GGAAAACAAGAGAAGCATCGAGGAAGTTCTGCCGGAGTTCCTCGGTTTTC | 1300 |
| TGGAAGATTCCATCATCGTAGCACACAACGCCAACTTCGACTACAGATTT | |
| CTGAGGCTGTGGATCAAAAAAGTGATGGGATTGGACTGGGAAAGACCCTA | 1400 |
| CATAGATACGCTCGCCCTCGCAAAGTCCCTTCTCAAACCTGAGAAGCTACT | |
| CTCTGGATTCCGTTGTGGAAAAGCTCGGATTGGGTCCCTTCCGGCACCAC | 1500 |
| AGGGCCCTGGATGACGCGAGGGTCACCGCTCAGGTTTTCTCAGGTTCTGT | |
| TGAGATGATGAAGAAGATCGGTATCACGAAGCTTTCAGAAATGGAGAAGT | 1600 |
| TGAAGGATACGATAGACTACACCGCGTTGAAACCCTTCCACTGCACGATC | |
| CTCGTTCAGAACAAAAAGGGATTGAAAAACCTATACAAACTGGTTTCTGA | 1700 |
| TTCTTATATAAAGTACTTCTACGGTGTTCGAGGATCCTCAAAAGTGAGC | |
| TCATCGAGAACAGAGAAGGACTGCTCGTGGGTAGCGCGTGTATCTCCGGT | 1800 |
| GAGCTCGGACGTGCCGCCCTCGAAGGAGCGAGTGATTTCAGAACTCGAAGA | |
| GATCGCGAAGTTCTACGACTACATAGAAGTCATGCCGCTCGACGTTATAG | 1900 |
| CCGAAGATGAAGAAGACCTAGACAGAGAAAGACTGAAAGAAGTGTACCGA | |
| AAACTCTACAGAATAGCGAAAAAATTGAACAAGTTCGTCGTCATGACCGG | 2000 |
| TGATGTTCAATTTCCCTCGATCCCGAAGATGCCAGGGGCAGAGCTGCACCTC | |
| TGGCACCTCAGGGAAACAGAACTTCGAGAATCAGCCCGCACTCTACCTC | 2100 |
| AGAACGACCGAAGAAATGCTCGAGAAGGCGATAGAGATATTCTGAAGATGA | |
| AGAGATCGCGAGGGGAAGTCGTGATAGAGAATCCCAACAGAATAGCCGATA | 2200 |
| TGATCGAGGAAGTGCAGCCGCTCGAGAAAAAATTCACCCGCCGATCATA | |
| GAGAACGCCGATGAAATAGTGAGAAACCTCACCATGAAGCGGGCGTACGA | 2300 |
| GATCTACGGTGATCCGCTTCCCGAAATCGTCCAGAAGCGTGTGGAAAAGG | |

FIG. 54A

REPLACEMENT SHEET

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| | |
|---|------|
| AACTGAACGCCATCATAAATCATGGATACGCCGTTCTCTATCTCATCGCT | 2400 |
| CAGGAGCTCGTTCAGAAATCTATGAGCGATGGTTACGTGGTTGGATCCAG | |
| AGGATCCGTCGGGTCTTCACTCGTGGCCAATCTCCTCGGAATAACAGAGG | 2500 |
| TGAATCCCCCTACCACCACATTACAGGTGTCCAGAGTGCAAATACTTTGAA | |
| GTTGTCGAAGACGACAGATACGGAGCGGGTTACGACCTTCCCAACAAGAA | 2600 |
| CTGTCCAAGATGTGGGGCTCCTCTCAGAAAAGACGGCCACGGCATAACCGT | |
| TTGAAACGTTTCATGGGGTTCGAGGGTGACAAGGTCCCCGACATAGATCTC | 2700 |
| AACTTCTCAGGAGAGTATCAGGAACGTGCTCATCGTTTGTGGAAGAACT | |
| CTTCGGTAAAGACCACGTCTATAGGGCGGGAACCATAAACACCATCGCGG | 2800 |
| AAAGAAGTGCGGTGGGTACGTGAGAAGCTACGAAGAGAAAACCGGAAAG | |
| AAGCTCAGAAAGGCGGAAATGGAAAGACTCGTTTCCATGATCACGGGAGT | 2900 |
| GAAGAGAACGACGGGTACGACCCAGGGGGGCTCATGATCATAACCGAAAG | |
| ACAAAGAAGTCTACGATTTCACTCCCATACAGTATCCAGCCAACGATAGA | 3000 |
| AACGCAGGTGTGTTACACACGCACTTCGCATACGAGACGATCCATGATGA | |
| CCTGGTGAAGATAGATGCGCTCGGCCACGATGATCCCACTTTCATCAAGA | 3100 |
| TGCTCAAGGACCTCACCGGAATCGATCCCATGACGATTCCCATGGATGAC | |
| CCCGATACGCTCGCCATATTCAGTTCTGTGAAGCCTCTTGGTGTGGATCC | 3200 |
| CGTTGAGCTGGAAAGCGATGTGGGAACGTACGGAATTCGGGAGTTCGGAA | |
| CCGAGTTTGTGAGGGGAATGCTCGTTGAAACGAGACCAAAGAGTTTCGCC | 3300 |
| GAGCTTGTGAGAATCTCAGGACTGTACACGGTACGGACGTCTGGTTGAA | |
| CAACGCACGTGATTGGATAAACCTCGGCTACGCCAAGCTCTCCGAGGTTA | 3400 |
| TCTCGTGTAGGGACGACATCATGAACTTCCTCATAACAAAGGAATGGAA | |
| CCGTCACTTGCCCTCAAGATCATGGAAAACGTACAGGAAGGGAAAGGTAT | 3500 |
| CACAGAAGAGATGGAGAGCGAGATGAGAAGGCTGAAGGTTCCAGAATGGT | |
| TCATCGAATCCTGTAAAAGGATCAAATATCTCTTCCCGAAAGCTCACGCT | 3600 |
| GTGGCTTACGTGAGTATGGCCTTCAGAATTGCTTACTTCAAGGTTCACTA | |
| TCCTCTTCAGTTTTACGCGGCGTACTTCACGATAAAAGGTGATCAGTTTCG | 3700 |
| ATCCGGTTCTCGTACTCAGGGGAAAAGAAGCCATAAAGAGGCGCTTGAGA | |
| GAACTCAAAGCGATGCCTGCCAAAGACGCCCAGAAGAAAAACGAAGTGAG | 3800 |
| TGTTCTGGAGGTTGCCCTGGAAATGATACTGAGAGGTTTTTCCTTCCTAC | |
| CGCCCGACATCTTCAAATCCGACGCGAAGAAATTTCTGATAGAAGGAAAC | 3900 |
| TCGCTGAGAATTCCGTTCAACAAACTTCCAGGACTGGGTGACAGCGTTGC | |
| CGAGTCGATAATCAGAGCCAGGGAAGAAAAGCCGTTCACTTCGGTGGAAG | 4000 |
| ATCTCATGAAGAGGACCAAGGTCAACAAAATCACATAGAGCTGATGAAA | |
| AGCCTGGGTGTTCTCGGGGACCTTCCAGAGACGGAACAGTTCACGCTTTT | 4100 |

C

FIG. 54B

REPLACEMENT SHEET

63/83

| | |
|--|------|
| MKKIENLKWKNVSFKSLEIDPDAGVVLVSVEKFSEEIEDLVRLLEKKTRF | |
| RVIVNGVQKSNGDLRGKILSLLNGNVPYIKDVVFEGNRLILKVLGDFARD | 100 |
| RIASKLRSTKKQLDELLPPGTEIMLEVVEPPEDLLKKEVPQPEKREEPKG | |
| EELKIEDENHIFGQKPRKIVFTPSKIFEYNKKTSVKGKIFKIEKIEGKRT | 200 |
| VLLIYLTGDGEDSLICKVFNDVEKVEGKVSVDVIVATGDLLLENGEPTLY | |
| VKGITKLPEAKRMDKSPVKRVELHAHTKFSDQDAITDVNEYVKRAKEWGF | 300 |
| PAIALTDHGNVQAIPIFYDAAKEAGIKPIFGIEAYLVSDVEPVIRNLSDD | |
| STFGDATFVVLDFETTGLDPQVDEIIIEIGAVKIQGGQIVDEYHTLIKPSR | 400 |
| EISRKSSEITGITQEMLENKRSIEEVLPEFLGFLEDSIIVAHNANFDYRF | |
| LRLWIKKVMGLDWERPDIIDTLALAKSLLKLSYSLDSVVEKLGLGPFRHH | 500 |
| RALDDARVTAQVFLRFVEMMKIGITKLSEMEKLDKDTIDYTALKPFHCTI | |
| LVQNKKGKLNLYKLVSDSYIKYFYGVPRILKSELINREGLLVGSACISG | 600 |
| ELGRAALEGASDSELEEIAKFYDYIEVMPLDVIAEDEEDLDRERLKEVYR | |
| KLYRIAKKLNKFVVMTGVDVHFLDPEDARGRAALLAPQGNRNFNENQPALYL | 700 |
| RTTEEMLEKAIEIFEDEEIAREVVNIENPNRIADMIEEVQPLEKKLHPPII | |
| ENADEIVRNLTMKRAYEIIYGDPLPEIVQKRVEKELNAINHGYAVLYLIA | 800 |
| QELVQKSMDSGYVVGSRGSSLVANLLGITEVNPLPPHYRCPECKYFE | |
| VVEDDRYGAGYDLPNKNCPRCGAPLRKDGHGIPFETFMGFEGDKVPDIDL | 900 |
| NFSGEYQERAHRFVEELFGKDHVYRAGTINTIAERSAVGYVRSYEEKTGK | |
| KLRKAEMERLVSMITGVKRTTGQHPGGLMIIPKDKEVYDFTPIQYPANDR | 1000 |
| NAGVFTTHFAYETIHDDLKIDALGHDDPTFIKMLKDLTGIDPMTIPMDD | |
| PDTLAIFSSVKPLGVDPELESDVGTYGIPEFGTEFVRGMLVETRPKSFA | 1100 |
| ELVRISGLSHGTDVWLNWARDWINLGYAKLSEVISCRDDIMNFLIHKGME | |
| PSLAFKIMENVRKGKGITEEMESEMRRLKVPEWFIESCRIKYLFPKAHA | 1200 |
| VAYVSMAFRIAYFKVHYPLQFYAAYFTIKGDQFDPVLVLRGKEAIIKRRLR | |
| ELKAMPAKDAQKKNEVSVLEVALEMILRGFSFLPPDIFKSDAKKFLIEGN | 1300 |
| SLRIPFNKLPGLGDSVAESIIRAREEKPFSTSVEDLMKRTKVKNKNIELMK | |
| SLGVLGDLPETEQFTLF | 1367 |

FIG. 55

REPLACEMENT
SHEET

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| | |
|---|-----|
| GTGCTCGCCATGATATGGAACGACACCGTTTTTTGCGTCGTAGACACAGA | |
| AACCACGGGAACCGATCCCTTTGCCGGAGACCGGATAGTTGAAATAGCCG | 100 |
| CTGTTCCCTGTCTTCAAGGGGAAGATCTACAGAAACAAAGCGTTTCACTCT | |
| CTCGTGAATCCCAGAATAAGAATCCCTGCGCTGATTCAGAAAGTTCACGG | 200 |
| TATCAGCAACATGGACATCGTGGAAGCGCCAGACATGGACACAGTTTACG | |
| ATCTTTTCAGGGATTACGTGAAGGGAACGGTGCTCGTGTTTCACAACGCC | 300 |
| AACTTCGACCTCACTTTTCTGGATATGATGGCAAAGGAAACGGGAACTT | |
| TCCAATAACGAATCCCTACATCGACACACTCGATCTTTCAGAAGAGATCT | 400 |
| TTGGAAGGCCTCATTCTCTCAAATGGCTCTCCGAAAGACTTGGAATAAAA | |
| ACCACGATACGGCACCGTGCTCTTCCAGATGCCCTGGTGACCGCAAGAGT | 500 |
| TTTTGTGAAGCTTGTTGAATTTCTTGGTGAAAACAGGGTCAACGAATTCA | |
| TACGTGGAAAACGGGGG | 567 |

FIG. 56

| | |
|--|-----|
| MLAMIWNDTVFCVVDTETTGTDPFAGDRIVEIAAVPVFKGKIYRNKAFHS | |
| LVNPRIRIPALIQKVHGISNMDIVEAPDMDTVYDLFRDYVKGTVLVFHNA | 100 |
| NFDLTFLDMMAKETGNFPITNPYIDTLDLSEEIFGRPHSLKWLSERLGIK | |
| TTIRHRALPDALVTARVFVKLVEFLGENRVNEFIRGKRG | 189 |

FIG. 57

REPLACEMENT SHEET

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| | |
|---|------|
| GTGGAAGTTCTTTACAGGAAGTACAGGCCAAAGACTTTTTCTGAGGTTGT | |
| CAATCAGGATCATGTGAAGAAGGCAATAATCGGTGCTATTCAGAAGAACA | 100 |
| GCGTGGCCACGGATACATATTCGCCGGTCCGAGGGGAACGGGGAAGACT | |
| ACTCTTGCCAGAATTCTCGCAAATCCCTGAACTGTGAGAACAGAAAGGG | 200 |
| AGTTGAACCTGCAATTCCTGCAGAGCCTGCAGAGAGATAGACGAGGGAA | |
| CCTTCATGGACGTGATAGAGCTCGACGCGGCCTCCAACAGAGGAATAGAC | 300 |
| GAGATCAGAAGAATCAGAGACGCCGTTGGATACAGGCCGATGGAAGGTAA | |
| ATACAAAGTCTACATAATAGACGAAGTTCACATGCTCACGAAAGAAGCCT | 400 |
| TCAACGCGCTCCTCAAAACACTCGAAGAACCCTCCTTCCCACGTCGTGTTT | |
| GTGCTGGCAACGACAAACCTTGAGAAGGTTCTTCCCACGATTATCTCGAG | 500 |
| ATGTCAGGTTTTTCGAGTTCAGAAACATTCCCGACGAGCTCATCGAAAAGA | |
| GGCTCCAGGAAGTTGCGGAGGCTGAAGGAATAGAGATAGACAGGGAAGCT | 600 |
| CTGAGCTTCATCGCAAAAAGAGCCTCTGGAGGCTTGAGAGACGCGCTCAC | |
| CATGCTCGAGCAGGTGTGGAAGTTCTCGGAAGGAAAGATAGATCTCGAGA | 700 |
| CGGTACACAGGGCGCTCGGGTTGATACCGATACAGGTTGTTTCGCGATTAC | |
| GTGAACGCTATCTTTTCTGGTGATGTGAAAAGGGTCTTACCAGTTCTCGA | 800 |
| CGACGTCTATTACAGCGGGAAGGACTACGAGGTGCTCATTTCAGGAAGCAG | |
| TCGAGGATCTGGTCGAAGACCTGGAAGGGGAGAGAGGGGTTTACCAGGTT | 900 |
| TCAGCGAACGATATAGTTTCAGGTTTCGAGACAACTTCTGAATCTTCTGAG | |
| AGAGATAAAGTTCGCCGAAGAAAAACGACTCGTCTGTAAAGTGGGTTTCGG | 1000 |
| CTTACATAGCGACGAGGTTCTCCACCACAAACGTTTCAGGAAAACGATGTC | |
| AGAGAAAAAACGATAATTCAAATGTACAGCAGAAAGAAGAGAAGAAAGA | 1100 |
| AACGGTGAAGGCAAAAGAAGAAAAACAGGAAGACAGCGAGTTCGAGAAAC | |
| GCTTCAAAGAACTCATGGAAGAACTGAAAGAAAAGGGCGATCTCTCTATC | 1200 |
| TTTGTGCTCTCAGCCTCTCAGAGGTGCAGTTTGACGGAGAAAAGGTGAT | |
| TATTTCTTTTGATTCATCGAAAGCTATGCATTACGAGTTGATGAAGAAAA | 1300 |
| AACTGCCTGAGCTGGAAAACATTTTTTCTAGAAAACTCGGGAAAAAAGTA | |
| GAAGTTGAACTTCGACTGATGGGAAAAGAAGAAACAATCGAGAAGGTTTC | 1400 |
| TCAGAAGATCCTGAGATTGTTTGAACAGGAGGGA | |

FIG. 58

| | |
|---|-----|
| MEVLYRKYPKTFSEVVNQDHSVKKAIIGAIQKNSVAHGYIFAGPRGTGKT | |
| TLARILAKSLNCENRKGVEPCNSCRACREIDEGTFMDVIELDAASNRGID | 100 |
| EIRRIRDAVGYPMEGKYKVYIIDEVHMLTKEAFNALLKTLEPPSHVVF | |
| VLATTNLEKVPPTIISRCQVFEFRNIPDELIEKRLQEVAAEGIEIDREA | 200 |
| LSFIAKRASGGLRDALTMLEQVWKFSEGGKIDLETVHRALGLIPIQVVRDY | |
| VNAIFSGDVKRFTVLDDVYYSKDYEVLIQEAVEDLVEDLERERGVYQV | 300 |
| SANDIVQVSRQLLNLLREIKFAEEKRLVCKVGSAYIATRFSTTNVQENDV | |
| REKNDNSNVQQKEKKETVKAKEEKQEDSEFEKRFKELMEELKEKGDLSI | 400 |
| FVALSLSEVQFDGEKVIIISFDSSKAMHYELMKKKLPELENIFSRKLGKKV | |
| EVELRLMGKEETIEKVSQKILRLFEQEG | 478 |

FIG. 59

REPLACEMENT SHEET

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| | |
|---|------|
| ATGAAAGTAACCGTCACGACTCTTGAATTGAAAGACAAAATAACCATCGC | |
| CTCAAAAGCGCTCGCAAAGAAATCCGTGAAACCCATTCTTGCTGGATTTC | 100 |
| TTTTTCGAAGTGAAAGATGGAAATTTCTACATCTGCGCGACCGATCTCGAG | |
| ACCGGAGTCAAAGCAACCGTGAATGCCGCTGAAATCTCCGGTGAGGCACG | 200 |
| TTTTGTGGTACCAGGAGATGTCATTGAGAAGATGGTCAAGGTTCTCCCAG | |
| ATGAGATAACGGAACTTTCTTTAGAGGGGGATGCTCTTGTTATAAGTTCT | 300 |
| GGAAGCACCGTTTTTCAGGATCACCACCATGCCCGCGGACGAATTTCCAGA | |
| GATAACGCCTGCCGAGTCTGGAATAACCTTCGAAGTTGACACTTCGCTCC | 400 |
| TCGAGGAAATGGTTGAAAAGGTCATCTTCGCCGCTGCCAAAGACGAGTTC | |
| ATGCGAAATCTGAATGGAGTTTTCTGGGAACTCCACAAGAATCTTCTCAG | 500 |
| GCTGGTTGCAAGTGATGGTTTCAGACTTGCACTTGCTGAAGAGCAGATAG | |
| AAAACGAGGAAGAGGCGAGTTTCTTGCTCTCTTTGAAGAGCATGAAAGAA | 600 |
| GTTCAAAACGTGCTGGACAACACAACGGAGCCGACTATAACGGTGAGGTA | |
| CGATGGAAGAAGGGTTTCTCTGTCGACAAATGATGTAGAAACGGTGATGA | 700 |
| GAGTGGTTCGACGCTGAATTTCCCGATTACAAAAGGGTGATCCCCGAACT | |
| TTCAAAACGAAAGTGGTGGTTTCCAGAAAAGAACTCAGGGAATCTTTGAA | 800 |
| GAGGGTGATGGTGATTGCCAGCAAGGGAAGCGAGTCCGTGAAGTTCGAAA | |
| TAGAAGAAAACGTTATGAGACTTGTGAGCAAGAGCCCGGATTATGGAGAA | 900 |
| GTGGTCGATGAAGTTGAAGTTCAAAAAGAAGGGGAAGATCTCGTGATCGC | |
| TTTCAACCCGAAGTTCATCGAGGACGTTTTGAAGCACATTGAGACTGAAG | 1000 |
| AAATCGAAATGAACTTCGTTGATTCTACCAGTCCATGTCAGATAAATCCA | |
| CTCGATATTTCTGGATACCTTTACATAGTGATGCCCATCAGACTGGCA | 1098 |

FIG. 60

| | |
|---|-----|
| MKVTVTTLLELKDKITIASKALAKKSVKPILAGFLFEVKDGNFYICATDLE | |
| TGVKATVNAAEISGEARFVVPGDVIQKMKVLPDEITELSLEGDALVISS | 100 |
| GSTVFRITTMPADEFPEITPAESGITFEVDTSLLEEMVEKVIFAAAKDEF | |
| MRNLNGVFWELHKNLLRLVASDGFRLALAEQIENEEEEEASFLLSLKSMKE | 200 |
| VQNVLDNTTEPTITVRYDGRRVSLSTNDVETVMRVVDAEFPDYKRVIPET | |
| FKTKVVVSRKELRESLKRVMVIAASKGSESVKFEIEENVMLVSKSPDYGE | 300 |
| VVDEVEVQKEGEDLVIAFNPKFIEDVLKHIETEEIEMNFVDSTSPCQINP | |
| LDISGYLYIVMPIRLA | 366 |

FIG. 61

REPLACEMENT SHEET

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| | |
|--|-----|
| ATGCCAGTCACGTTTCTCACAGGTACTGCAGAACTCAGAAGGAAGAATT | |
| GATAAAGAACTCCTGAAGGATGGTAACGTGGAGTACATAAGGATCCATC | 100 |
| CGGAGGATCCCGACAAGATCGATTTTCATAAGGTCTTTACTCAGGACAAAG | |
| ACGATCTTTTCCAACAAGACGATCATTGACATCGTCAATTTTCGATGAGTG | 200 |
| GAAAGCACAGGAGCAGAAGCGTCTCGTTGAACTTTTGAAAAACGTACCGG | |
| AAGACGTTTCATATCTTCATCCGTTCTCAAAAAACAGGTGGAAAGGGAGTA | 300 |
| GCGCTGGAGCTTCCGAAGCCATGGGAAACGGACAAGTGGCTTGAGTGGAT | |
| AGAAAAGCGCTTCAGGGAGAATGGTTTGCTCATCGATAAAGATGCCCTTC | 400 |
| AGCTGTTTTTCTCCAAGGTTGGAACGAACGACCTGATCATAGAAAGGGAG | |
| ATTGAAAAACTGAAAGCTTATTCCGAGGACAGAAAGATAACGGTAGAAGA | 500 |
| CGTGGAAGAGGTCGTTTTTACCTATCAGACTCCGGGATACGATGATTTTT | |
| GCTTTGCTGTTTCCGAAGGAAAAAGGAAGCTCGCTCACTCTCTTCTGTCTG | 600 |
| CAGCTGTGGAAGAACACAGAGTCCGTGGTGATTGCCACTGTCCTTGCGAA | |
| TCACTTCTTGATCTCTTCAAAATCCTCGTTCTTGTGACAAAGAAAAGAT | 700 |
| ACTACACCTGGCCTGATGTGTCCAGGGTGTCCAAAGAGCTGGGAATTCCC | |
| GTTCCCTCGTGTGGCTCGTTTCCCTCGGTTTCTCCTTTAAGACCTGGAAATT | 800 |
| CAAGGTGATGAACCACCTCCTCTACTACGATGTGAAGAAGGTTAGAAAGA | |
| TACTGAGGGATCTCTACGATCTGGACAGAGCCGTGAAAAGCGAAGAAGAT | 900 |
| CCAAAACCGTTCTTCCACGAGTTCATAGAAGAGGTGGCACTGGATGTATA | |
| TTCTCTTCAGAGAGATGAAGAA | 972 |

FIG. 62

| | |
|---|-----|
| MPVTFLTGTAEQKEELIKLLKDGNEVEYIRIHPEDPDKIDFIRSLLRTK | |
| TIFSNTIIDIVNFDEWKAQEQKRLVELLKNVPEDVHIFIRSQKTGGKGV | 100 |
| ALELPKPWETDKWLEWIEKRFRENGLLIDKDALQLFFSKVGTNDLI IERE | |
| IEKLKAYSEDRKITVEDVEEVVFTYQTPGYDDFCFAVSEGKRKLAHSLLS | 200 |
| QLWKTTESVVIATVLANHFLDLFKILVLVTKKRYYTWPDVSRVSKELGIP | |
| VPRVARFLGFSFKTWKFKVMNHLLYYDVKKVRKILRDLYDLDRVAVKSEED | 300 |
| PKPFFHEFIEEVALDVYSLQRDEE | |

FIG. 63

REPLACEMENT
SHEET

68/83

| | |
|---|-----|
| ATGAACGATTTGATCAGAAAGTACGCTAAAGATCAACTGGAACTTTGAA | |
| AAGGATCATAGAAAAGTCTGAAGGAATATCCATCCTCATAAATGGAGAAG | 100 |
| ATCTCTCGTATCCGAGAGAAGTATCCCTTGAACCTCCCGAGTACGTGGAG | |
| AAATTTCCCCCGAAGGCCTCGGATGTTCTGGAGATAGATCCCGAGGGGGA | 200 |
| GAACATAGGCATAGACGACATCAGAACGATAAAGGACTTCCTGAACTACA | |
| GCCCCGAGCTCTACACGAGAAAGTACGTGATAGTCCACGACTGTGAAAGA | 300 |
| ATGACCCAGCAGGCGGCGAACGCGTTTCTGAAGGCCCTTGAAGAACCACC | |
| AGAATACGCTGTGATCGTTCTGAACACTCGCCGCTGGCATTATCTACTGC | 400 |
| CGACGATAAAGAGCCGAGTGTTTCAGAGTGGTTGTGAACGTTCCAAAGGAG | |
| TTCAGAGATCTCGTGAAAGAGAAAATAGGAGATCTCTGGGAGGAACTTCC | 500 |
| ACTTCTTGAGAGAGACTTCAAAACGGCTCTCGAAGCCTACAACTTGGTG | |
| CGGAAAAAATTTCTGGATTGATGGAAAGTCTCAAAGTTTTGGAGACGGAA | 600 |
| AAACTCTTGAAAAAGGTCCTTTCAAAGGCCCTCGAAGGTTATCTCGCATG | |
| TAGGGAGCTCCTGGAGAGATTTTCAAAGGTGGAATCGAAGGAATTCTTTG | 700 |
| CGCTTTTTTGATCAGGTGACTAACACGATAACAGGAAAAGACGCGTTTCTT | |
| TTGATCCAGAGACTGACAAGAATCATTCTCCACGAAAACACATGGGAAAG | 800 |
| CGTTGAAGATCAAAAAAGCGTGTCTTTCCTCGATTCAATTCTCAGGGTGA | |
| AGATAGCGAATCTGAACAACAACTCACTCTGATGAACATCCTCGCGATA | 900 |
| CACAGAGAGAGAAAGAGAGGTGTCAACGCTTGGAGC | |

FIG. 64

| | |
|--|-----|
| MNDLIRKYAKDQLETLKRIIEKSEGISILINGEDLSYPREVSLELPEYVE | |
| KFPPKASDVLEIDPEGENIGIDDIRTIKDFLNYSPELYTRKYVIVHDCER | 100 |
| MTQQAANAFLKALEEPPEYAVIVLNTRRWHYLLPTIKSRVFRVVVNPKE | |
| FRDLVKEKIGDLWEELPLLERDFKTALEAYKLGAEKLSGLMESLKVLETE | 200 |
| LLKKVLSKGLEGYLACRELLERFSKVESKEFFALFDQVTNTITGKDAFL | |
| LIQRLTRIILHENTWESVEDKSVSFLDSILRVKIANLNNKLTLMNILAIH | 300 |
| RERKRGVNAWS | |

FIG. 65

REPLACEMENT
SHEET

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ATGTCTTTCTTCAACAAGATCATACTCATAGGAAGACTCGTGAGAGATCC
CGAAGAGAGATACACGCTCAGCGGAACTCCAGTCACCACCTTCACCATAG 100
CGGTGGACAGGGTTCCCAGAAAGAACGCGCCGGACGACGCTCAAACGACT
GATTTCTTCAGGATCGTCACCTTTGGAAGACTGGCAGAGTTCGCTAGAAC 200
CTATCTCACCAAAGGAAGGCTCGTTCTCGTCGAAGGTGAAATGAGAATGA
GAAGATGGGAAACACCCACTGGAGAAAAGAGGGTATCTCCGGAGGTTGTC 300
GCAAACGTTGTTAGATTCATGGACAGAAAACCTGCTGAAACAGTTAGCGA
GACTGAAGAGGAGCTGGAAATACCGGAAGAAGACTTTTCCAGCGATACCT 400
TCAGTGAAGATGAACCACCATT

FIG. 66

MSFFNKIILIGRLVRDPEERYTLSGTPVTTFTIAVDRVPRKNAPDDAQT
DFFRIVTFGRLAEFARTYLTGRLVLVEGEMRMRWETPTGEKRVSPVV 100
ANVVRFMDRKPAETVSETEEELEIPEEDFSSDTFSEDEPPF

FIG. 67

REPLACEMENT SHEET

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| | |
|---|------|
| ATGCGTGTCCCCCGCACAACTTAGAGGCCGAAGTTGCTGTGCTCGGAAG | |
| CATATTGATAGATCCGTCCGTAATAAACGACGTTCTTGAAATTTTGAGCC | 100 |
| ACGAAGATTTCTATCTGAAAAAACACCAACACATCTTCAGAGCGATGGAA | |
| GAGCTTTACGACGAAGGAAAACCGGTGGACGTGGTTTCCGTCTGTGACAA | 200 |
| GCTTCAAAGCATGGGAAAACCTCGAGGAAGTAGGTGGAGATCTGGAAGTGG | |
| CCCAGCTCGCTGAGGCTGTGCCAGTTCTGCACACGCACTTCACTACGCG | 300 |
| GAGATCGTCAAGGAAAAATCCATTCTGAGGAACTCATTGAGATCTCCAG | |
| AAAAATCTCAGAAAGTGCCTACATGGAAGAAGATGTGGAGATCCTGCTCG | 400 |
| ACAACGCAGAAAAGATGATCTTCGAGATCTCAGAGATGAAAACGACAAAA | |
| TCCTACGATCATCTGAGAGGCATCATGCACCGGGTGTGTTGAAAACCTGGA | 500 |
| GAACCTCAGGGAAAGAGCCAACTTATAGAACCCGGTGTGCTCATAACGG | |
| GACTACCAACGGGATTCAAAGTCTGGACAAACAGACCACAGGGTTCCAC | 600 |
| AGCTCCGATCTGGTGATAATAGCAGCGAGACCCCTCCATGGGAAAAACCTC | |
| CTTCGCACTCTCAATAGCGAGGAACATGGCTGTCAATTTCGAAATCCCCG | 700 |
| TCGGAATATTCAGTCTCGAGATGTCCAAGGAACAGCTCGCTCAAAGACTA | |
| CTCAGCATGGAGTCCGGTGTGGATCTTTACAGCATCAGAACAGGATACCT | 800 |
| GGATCAGGAGAAGTGGGAAAGACTCACAATAGCGGCTTCTAAACTCTACA | |
| AAGCACCCATAGTTGTGGACGATGAGTCACTCCTCGATCCGCGATCGTTG | 900 |
| AGGGCAAAAGCGAGAAGGATGAAAAAAGAATACGATGTAAAAGCCATTTT | |
| TGTCGACTATCTCCAGCTCATGCACCTGAAAGGAAGAAAAGAAAGCAGAC | 1000 |
| AGCAGGAGATATCCGAGATCTCGAGATCTCTGAAGCTCCTTGCGAGGGAA | |
| CTCGACATAGTGGTGATAGCGCTTTCACAGCTTTCGAGGGCCGTAGAACA | 1100 |
| GAGAGAAGACAAAAGACCGAGGCTGAGTGACCTCAGGGAATCCGGTGCGA | |
| TAGAACAGGACGCAGACACAGTCATCTTCATCTACAGGGAGGAATATTAC | 1200 |
| AGGAGCAAAAAATCCAAAGAGGAAAGCAAGCTTCACGAACCTCACGAAGC | |
| TGAAATCATAATAGGTAAACAGAGAAACGGTCCCGTTGGAACGATCACTC | 1300 |
| TGATCTTCGACCCCAGAACGGTTACGTTCCATGAAGTCGATGTGGTGCAT | |
| TCA | 1353 |

FIG. 68

| | |
|---|-----|
| MRVPPHNLEAEVAVLGSILIDPSVINDVLEILSHEDFYLLKKHQHIFRAME | |
| ELYDEGKPVVDVSVCDKLQSMGKLEEVGGDLEVAQLAEAVPSSAHALHYA | 100 |
| EIVKEKSILRKLIIEISRKISESAYMEEDVEILLDNAEKMIFEISEMKTTK | |
| SYDHLRGIMHRVFENLENFRERANLIEPGVLITGLPTGFKSLDKQTTGFH | 200 |
| SSDLVIIAARPSMGKTSFALSIARNMAVNFEIPVGIFSLEMSKEQLAQRL | |
| LSMESGVDLYSIRTGYLDQEKWERLTIAASKLYKAPIVVDDESLLDPRSL | 300 |
| RAKARRMKKEYDVKAIFVDYLQLMHLKGRKESRQQEISEISRSLKLLARE | |
| LDIVVIALSQLSRAVEQREDKRPRLSDLRESGAIEQDADTVIFIFYREEYY | 400 |
| RSKKSKEESKLHEPHEAEIIIGKQRNGPVGTTITLIFDPRTVTFHEVDVH | |
| S | 451 |

FIG. 69

REPLACEMENT SHEET

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| | |
|--|------|
| GTGATTCCCTCGAGAGGTCATCGAGGAAATAAAAGAAAAGGTTGACATCGT | |
| AGAGGTCATTTCCGAGTACGTGAATCTTACCCGGGTAGGTTCCCTCCTACA | 100 |
| GGGCTCTCTGTCCCTTTCATTTCAGAAACCAATCCTTCTTTCTACGTTTCAT | |
| CCGGGTTTGAAGATATAACCATTTGTTTCGGCTGCGGTGCGAGTGGAGACGT | 200 |
| CATCAAATTTCTTCAAGAAATGGAAGGGATCAGTTTCCAGGAAGCGCTGG | |
| AAAGACTTGCCAAAAGAGCTGGGATTGATCTTTCTCTCTACAGAACAGAA | 300 |
| GGGACTTCTGAATACGGAAAATACATTCGTTTGTACGAAGAAACGTGGAA | |
| AAGGTACGTCAAAGAGCTGGAGAAATCGAAAGAGGCAAAAGACTATTTAA | 400 |
| AAAGCAGAGGGCTTCTCTGAAGAAGATATAGCAAAGTTCGGCTTTGGGTAC | |
| GTCCCCAAGAGATCCAGCATCTCTATAGAAGTTGCAGAAGGCATGAACAT | 500 |
| AACACTGGAAGAACTTGTCAGATACGGTATCGCGCTGAAAAAGGGTGATC | |
| GATTCGTTGATAGATTCGAAGGAAGAATCGTTGTTCCAATAAAGAACGAC | 600 |
| AGTGGTCATATTGTGGCTTTTGGTGGGCGTGCTCTCGGCAACGAAGAACC | |
| GAAGTATTTGAACTCTCCAGAGACCAGGTATTTTTCGAAGAAGAAGACCC | 700 |
| TTTTTCTCTTCGATGAGGCGAAAAAAGTGGCAAAAGAGGTTGGTTTTTTC | |
| GTCATCACCGAAGGCTACTTCGACGCGCTCGCATTTCAGAAAGGATGGAAT | 800 |
| ACCAACGGCGGTCGCTGTTCTTGGGGCGAGTCTTTCAAGAGAGGCGATTTC | |
| TAAAACCTTTCGGCGTATTCGAAAAACGTCATACTGTGTTTCGATAATGAC | 900 |
| AAAGCAGGCTTCAGAGCCACTCTCAAATCCCTCGAGGATCTCCTAGACTA | |
| CGAATTCAACGTGCTTGTGGCAACCCCCCTCTCCTTACAAAGACCCAGATG | 1000 |
| AACTCTTTCAGAAAGAAGGAGAAGGTTTCATTGAAAAAGATGCTGAAAAAC | |
| TCGCGTTTCGTTTCGAATATTTTCTGGTGACGGCTGGTGAGGTCTTCTTTGA | 1100 |
| CAGGAACAGCCCCGCGGGTGTGAGATCCTACCTTTCTTTCTCCTCAAAGGTT | |
| GGGTCCAAAAGATGAGAAGGAAAGGATATTTGAAACACATAGAAAATCTC | 1200 |
| GTGAATGAGGTTTCATCTTCTCTCCAGATACCAGAAAACCAGATTTTGAA | |
| CTTTTTTGAAGCGACAGGTCTAACACTATGCCTGTTTCATGAGACCAAGT | 1300 |
| CGTCAAAGGTTTACGATGAGGGGAGAGGACTGGCTTATTTGTTTTTGAAC | |
| TACGAGGATTTGAGGGAAAAGATTCTGGAAGTGGACTTAGAGGTACTGGA | 1400 |
| AGATAAAAACGCGAGGGAGTTTTTCAAGAGAGTCTCACTGGGAGAAGATT | |
| TGAACAAAGTCATAGAAAACCTCCCAAAGAGCTGAAAGACTGGATTTTTT | 1500 |
| GAGACAATAGAAAGCATTCCTCCTCCAAAGGATCCCGAGAAATTCCTCGG | |
| TGACCTCTCCGAAAAGTTGAAAATCCGACGGATAGAGAGACGTATCGCAG | 1600 |
| AAATAGATGATATGATAAAGAAAGCTTCAAACGATGAAGAAAGGCGTCTT | |
| CTTCTCTCTATGAAAGTGGATCTCCTCAGAAAAATAAAGAGGAGG | 1695 |

FIG. 70

REPLACEMENT SHEET

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| | |
|---|-----|
| MIPREVIEEIKEKV DIVEVISEYVNLTRVGSSYRALCPFHSETNPSFYVH | |
| PGLKIYHCFGCGASGDVIKFLQEMEGISFQEALERLAKRAGIDLSLYRTE | 100 |
| GTSEYGKYIRLYEETWKRYVKELEKSKEAKDYLSRGFSEEDIAKFGFGY | |
| VPKRSSISIEVAEGMNITLEELVRYGIALKKGDRFVDRFEGRIVVPIKND | 200 |
| SGHIVAFGGRALGNEEPKYLNSPETRYFSKKKTLFLFDEAKKVAKEVGFF | |
| VITEGYFDALAFRKDGIPTAVAVLGASLSREAILKLSAYSKNVILCFDND | 300 |
| KAGFRATLKSLEDLLDYEFNVLVATPSPYKDPDELFOKEGEGSLKKMLKN | |
| SRSFEYFLVTAGEVFFDRNSPAGVRSYLSFLKGWVQKMRRKGYLKHENL | 400 |
| VNEVSSSLQIPENQILNFFESDRSNTMPVHETKSSKVYDEGRGLAYLFLN | |
| YEDLREKILELDLEVLEDKNAREFFKRVSLGEDLNKVIENFPKELKDWIF | 500 |
| ETIESIPPPKDPEKFLGDLSEKLKIRRIERIAEIDDMIKKASNDEERRL | |
| LLSMKVDLLRKIKRR | 565 |

FIG. 71

| | |
|--|-----|
| ATGGCTCTACACCCGGCTCACCCTGGGGCAATAATCGGGCACGAGGCCGT | |
| TCTCGCCCTCCTTCCCCGCCTCACCGCCAGACCCTGCTCTTCTCCGGCC | 100 |
| CCGAGGGGGTGGGGCGGCGCACCGTGCGCCGCTGGTACGCCTGGGGGCTC | |
| AACCGCGGCTTCCCCCGCCCTCCCTGGGGGAGCACCCGGACGTCTCTCGA | 200 |
| GGTGGGGCCCAAGGCCCGGGACCTCCGGGGCCGGGCGAGGTGCGGCTGG | |
| AGGAGGTGGCGCCCCCTCTTGAGTGCTGCCAGCCACCCCCGGGAGCGG | 300 |
| GTGAAGGTGGCCATCCTGGACTCGGCCCACCTCCTCACCAGGCCGCGGC | |
| CAACGCCCTCCTCAAGCTCCTGGAGGAGCCCCCTCCTACGCCCGCATCG | 400 |
| TCCTCATCGCCCCAAGCCGCGCCACCCTCCTCCCCACCCTGGCCTCCCGG | |
| GCCACGGAGGTGGCATTCGCCCCCGTGCCCGAGGAGGCCCTGCGCGCCCT | 500 |
| CACCCAGGACCCGGAGCTCCTCCGCTACGCCGCGGGGCCCCGGGCGCC | |
| TCCTTAGGGCCCTCCAGGACCCGGAGGGGTACCGGGCCCGCATGGCCAGG | 600 |
| GCGCAAAGGGTCTTGAAAGCCCCGCCCTGGAGCGCCTCGCTTTGCTTCG | |
| GGAGCTTTTGGCCGAGGAGGAGGGGGTCCACGCCCTCCACGCCGTCCTAA | 700 |
| AGCGCCCGGAGCACCTCCTTGCCCTGGAGCGGGCGCGGGAGGCCCTGGAG | |
| GGGTACGTGAGCCCCGAGCTGGTCCTCGCCCGGCTGGCCTTAGACTTAGA | 800 |
| GACA | |

FIG. 72

| | |
|---|-----|
| MALHPAHPGAIIGHEAVLALLPRLTAQTLLFSGPEGVGRRTVARWYAWGL | |
| NRGFPPPSLGEHPDVLEVGPKARDLRGRAEVRLEEVAPLLEWCSSHPRER | 100 |
| VKVAILDSAHLLTEAAANALLKLEEPSYARIVLIAPSRATLLPTLASR | |
| ATEVAFAPVPEEALRALTQDPELLRYAAGAPGRLLRALQDPEGYRARMAR | 200 |
| AQRVLKAPPLERLALLRELLAE EEGVHALHAVLKRPEHLLALERAREALE | |
| GYVSPELVLARLALDLET | 268 |

FIG. 73

REPLACEMENT
SHEET

73/83

| | |
|--|-----|
| ATGCTGGACCTGAGGGAGGTGGGGGAGGCGGAGTGGAAGGCCCTAAAGCC | |
| CCTTTTGGAAGCGTGCCCGAGGGCGTCCCGTCCCTCCTGACCCCTA | 100 |
| AGCCAAGCCCCCTCCCGGGCGGCCTTCTACCGGAACCGGGAAAGGCGGGAC | |
| TTCCCCACCCCCAAGGGGAAGGACCTGGTGCGGCACCTGGAAAACCGGGC | 200 |
| CAAGCGCCTGGGGCTCAGGCTCCCGGGCGGGGTGGCCCAGTACCTGGCCT | |
| CCCTGGAGGGGGACCTCGAGGCCCTGGAGCGGGAGCTGGAGAAGCTTGCC | 300 |
| CTCCTCTCCCCACCCCTCACCCCTGGAGAAGGTGGAGAAGGTGGTGGCCCT | |
| GAGGCCCCCCCCCTCACGGGCTTTGACCTGGTGCGCTCCGTCCTGGAGAAGG | 400 |
| ACCCCAAGGAGGCCCTCCTGCGCCTAGGCGGCCTCAAGGAGGAGGGGGAG | |
| GAGCCCCCTCAGGCTCCTCGGGGCCCTCTCCTGGCAGTTCGCCCTCCTCGC | 500 |
| CCGGGCCTTCTTCCTCCTCCGGGAAAACCCCAAGGAGGAGGACC | |
| TCGCCCCGCTCGAGGCCACCCCTACGCCGCCCGCCGCGCCCTGGAGGCG | 600 |
| GCGAAGCGCCTCACGGAAGAGGCCCTCAAGGAGGCCCTGGACGCCCTCAT | |
| GGAGGCGGAAAAGAGGGCCAAGGGGGGGAAAGACCCGTGGCTCGCCCTGG | 700 |
| AGGCGGCGGTCTCCGCCTCGCCCGTTGA | |

FIG. 74

| | |
|---|-----|
| MVIAFTGDPFLAREALLEEARLRGLSRFTEPTPEALAQALAPGLFGGGGA | |
| MLDLREVGEAEWKALKPLLESVPEGVPVLLLDPKPSPSRAAFYRNRERRD | 100 |
| FPTPKGKDLVRHLENRAKRLGLRPLPGGVAQYLASLEGDLEALERELEKLA | |
| LLSPPLTLEKVEKVVALRPPLTGFDLVRVLEKDPKEALLRLGGLKEEGE | 200 |
| EPLRLLGALSWQFALLARAFFLLRENPRPKEEDLARLEAHPYAARRALEA | |
| AKRLTEEALKEALDALMEAEKRAKGKDPWLALEAAVLRRLAR | 292 |

FIG. 75

REPLACEMENT
SHEET

74/83

| | |
|---|-----|
| ATGGCTCGAGGCCTGAACCGCGTTTTTCCTCATCGGCGCCCTCGCCACCCG | |
| GCCGGACATGCGCTACACCCCGCGGGGCTCGCCATTTTGGACCTGACCC | 100 |
| TCGCCGGTCAGGACCTGCTTCTTTCCGATAACGGGGGGGAACCGGAGGTG | |
| TCCTGGTACCACCGGGTGAGGCTCTTAGGCCGCCAGGCGGAGATGTGGGG | 200 |
| CGACCTCTTGGACCAAGGGCAGCTCGTCTTCGTGGAGGGCCGCTGGAGT | |
| ACCGCCAGTGGGAAAGGGAGGGGGAGAAGCGGAGCGAGCTCCAGATCCGG | 300 |
| GCCGACTTCCGGACCCCCTGACGACCGGGGGAAGAAGCGGGCGGAGGAC | |
| AGCCGGGGCCAGCCCAGGCTCCGCGCCGCCCTGAACCAGGTCTTCCTCAT | 400 |
| GGGCAACCTGACCCGGGACCCGGAACCTCCGCTACACCCCCAGGGCACCG | |
| CGGTGGCCCGGCTGGGCCTGGCGGTGAACGAGCGCCGCCAGGGGGCGGAG | 500 |
| GAGCGCACCCACTTCGTGGAGGTTTACGGCCTGGCGCGACCTGGCGGAGTG | |
| GGCCGCCGAGCTGAGGAAGGGCGACGGCCTTTTCGTGATCGGCAGGTTGG | 600 |
| TGAACGACTCCTGGACCAGCTCCAGCGCGAGCGGCGCTTCCAGACCCGT | |
| GTGGAGGCCCTCAGGCTGGAGCGCCCCACCCGTGGACCTGCCCAGGCCTG | 700 |
| CCCAGGCCGGCGGAACAGGTCCCGCGAAGTCCAGACGGGTGGGGTGGACA | |
| TTGACGAAGGCTTGAAGACTTTCGCGCGGAGGAGGATTTGCCGTTTTGA | 800 |
| GCACGAA | |

FIG. 76

| | |
|--|-----|
| MARGLNRVFLIGALATRPDMRYTPAGLAILDLTLAQDLLLLSDNGGEPEV | |
| SWYHRVRLLG RQAEMWGDLDDQGQLVFVEGRLEYRQWEREGEKRSELQIR | 100 |
| ADFLDPLDDRGGKKRAEDSRGQPRRLRAALNQVFLMGNLTRDPELRYTPQGT | |
| AVARLGLAVNERRQGAEERTHFVEVQAWRDLAEWAAELRKGDGLFVIGRL | 200 |
| VNDSWTSSSGERRFQTRVEALRLERPTRGPAQACPGRRNRSREVQTGGVD | |
| IDEGLEDFPPEEDLPF | 266 |

FIG. 77

REPLACEMENT SHEET

75/83

| | |
|---|-----|
| AATTCCGACATTTCAATTGAATCGTTTATTCCGCTTGAAAAAGAAGGCAA | |
| GTTGCTCGTTGATGTGAAAAGACCGGGGAGCATCGTACTGCAGGCGCGCT | 100 |
| TTTTCTCTGAAATCGTGAAAAAACTGCCGCAACAAACGGTGGAATCGAA | |
| ACGGAAGACAACCTTTTTGACGATCATCCGCTCGGGGCACTCAGAATTCCG | 200 |
| CCTCAATGGGCTAAACGCCGACGAATATCCGCGCCTGCCGCAAATTGAAG | |
| AAGAAAACGTGTTTCAAATCCCGGCTGATTTATTGAAAACCGTGATTTCGG | 300 |
| CAAACGGTGTTTCGCCGTTTCTACATCGGAAACGCGCCCAATCTTGACAGG | |
| TGTCAACTGGAAAGTTGAACATGGCGAGCTTGTCTGCACAGCGACCGACA | 400 |
| GTCATCGCTTAGCCATGCGCAAAGTGAAAATTGAGTCGGAAAATGAAGTA | |
| TCATACAACGTCGTCATCCCTGGA AAAAGTCTTAATGAGCTCAGCAAAAT | 500 |
| TTTGGATGACGGCAACCACCCGGTGGACATCGTCATGACAGCCAATCAAG | |
| TGCTATTTAAGGCCGAGCACCTTCTCTTCTTTTCCCGGCTGCTTGACGGC | 600 |
| AACTATCCGGAGACGGCCCGCTTGATTCCAACAGAAAGCAAAACGACCAT | |
| GATCGTCAATGCAAAAGAGTTTCTGCAGGCAATCGACCGAGCGTCCTTGC | 700 |
| TTGCTCGAGAAGGAAGGAACAACGTTGTGAAACTGACGACGCTTCCTGGA | |
| GGAATGCTCGAAATTTCTTCGATTTCTCCGAGATCGGGAAAGTGACGGAG | 800 |
| CAGCTGCAAACGGAGTCTCTTGAAGGGGAAGAGTTGAACATTTTCGTTTCA | |
| CGCGAAATATATGATGGACGCGTTGCGGGCGCTTGATGGAACAGACATTT | 900 |
| CAAATCAGCTTCACTGGGGCCATGCGGCCGTTCTGTTGCGCCCGCTTCA | |
| ACCGATTGATGCTTCAGCTCATTTTGCCGGTGAGAACATAT | 992 |

FIG. 78

| | |
|---|-----|
| NSDISIIESFIPLEKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEI | |
| ETEDNFLTIIRSGHSEFRLNGLNADEYPRLPQIEEENVFQIPADLLKTVI | 100 |
| RQTVFAVSTSETRPILTG VNWKVEHGELVCTATDSHRLAMRKVKIIESEN | |
| EVSYNVVI PGKSLNELSKIILDDGNHPVDIVMTANQVLFKAEHLLFFSRL | 200 |
| LDGNYPETARLIPTESKTTMIVNAKEFLQ AIDRASLLAREGRNNVVKLTT | |
| LPGGMLEISSISPEIGKVTEQLQTESLEGEELNISFS AKYMMDALRALDG | 300 |
| TDIQISFTGAMRPFLLRPLHTDSMLQLILPVRTY | |

FIG. 79

REPLACEMENT
SHEET

76/83

| | |
|---|-----|
| ATGATTAACCGCGTCATTTTGGTCGGCAGGTAAACGAGAGATCCGGAGTT | |
| GCGTTACACTCCAAGCGGAGTGGCTGTTGCCACGTTTACGCTCGCGGTCA | 100 |
| ACCGTCCGTTTACAAATCAGCAGGGCGAGCGGGAAACGGATTTTATTCAA | |
| TGTGTCGTTTGGCGCCGCCAGGCGGAAAACGTCGCCAACTTTTGA AAAA | 200 |
| GGGGAGCTTGGCTGGTGTTCGATGGCCGACTGCAAACCCGCAGCTATGAAA | |
| ATCAAGAAGGTCGGCGTGTGTACGTGACGGAAGTGGTGGCTGATAGCGTC | 300 |
| CAATTTCTTGAGCCGAAAGGAACGAGCGAGCAGCGAGGGGCGACAGCAGG | |
| CGGCTACTATGGGGATCCATTCCCATTTCGGGCAAGATCAGAACCACCAAT | 400 |
| ATCCGAACGAAAAAGGGTTTGGCCGCATCGATGACGATCCTTTCGCCAAT | |
| GACGGCCAGCCGATCGATATTTCTGATGATGATTTGCCGTTT | 492 |

FIG. 80

| | |
|--|-----|
| MINRVILVGRLTRDPELRYTPSGVAVATFTLAVNRPFTNQSYENQEGRRV | |
| YVTEVVADSVQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRRQAEN | 100 |
| VANFLKKGSLAGVDGRLQTRGDPFPFGQDQNHQYPNEKGFGRIDDDPFAN | |
| DGQPIDISDDDLPF | 164 |

FIG. 81

REPLACEMENT SHEET

77/83

| | |
|---|------|
| ATGCTGGAACGCGTATGGGGAAACATTGAAAAACGGCGTTTTTCTCCCCT | |
| TTATTTATTATACGGCAATGAGCCGTTTTTATTAACGGAAACGTATGAGC | 100 |
| GATTGGTGAACGCAGCGCTTGGCCCCGAGGAGCGGGAGTGGAAC TTGGCT | |
| GTGTACGACTGCGAGGAAACGCCGATCGAGGCGGCGCTTGAGGAGGCCGA | 200 |
| GACGGTGCCGTTTTTTCGGCGAGCGGCGTGTCATTCTCATCAAGCATCCAT | |
| ATTTTTTTACGTCTGAAAAAGAGAAGGAGATCGAACATGATTTGGCGAAG | 300 |
| CTGGAGGCGTACTTGAAGGCGCCGTCGCCGTTTTTCGATCGTCGTCTTTTT | |
| CGCGCCGTACGAGAAGCTTGATGAGCGAAAAAAATTACGAAGCTCGCCA | 400 |
| AAGAGCAAAGCGAAGTCGTCATCGCCGCCCGCTCGCCGAAGCGGAGCTG | |
| CGTGCCTGGGTGCGGCGCCGCATCGAGAGCCAAGGGGCGCAAGCAAGCGA | 500 |
| CGAGGCGATTGATGTCCTGTTGCGGCGGGCGGGACGCAGCTTTCGCGCT | |
| TGGCGAATGAAATCGATAAATTGGCCCTGTTTGCCGGATCGGGCGGAACC | 600 |
| ATCGAGGCGGCGGCGGTTGAGCGGCTTGTCGCCCGCACGCCGGAAGAAAA | |
| CGTATTTGTGCTTGTCGAGCAAGTGGCGAAGCGCGACATTCCAGCAGCGT | 700 |
| TGCAGACGTTTTTATGATCTGCTTGAAAACAATGAAGAGCCGATCAAAATT | |
| TTGGCGTTGCTCGCCGCCCATTTCCGCTTGCTTTCGCAAGTGAAATGGCT | 800 |
| TGCCTCCTTAGGCTACGGACAGGCGCAAATTGCTGCGGCGCTCAAGGTGC | |
| ACCCGTTCCGCGTCAAGCTCGCTCTTGCTCAAGCGGCCCGCTTCGCTGAC | 900 |
| GGAGAGCTTGCTGAGGCGATCAACGAGCTCGCTGACGCCGATTACGAAGT | |
| GAAAAGCGGGGCGGTGATCGCCGTTGGCCGTTGAGCTGCTTCTGATGC | 1000 |
| GCTGGGGCGCCCGCCGGCGCAAGCGGGGCGCCACGGCCGGCGG | |

FIG. 82

| | |
|---|-----|
| MLERVWGNIEKRRFSPLYLLYGNPFLLTETYERLVNAALGPEEREWNLA | |
| VYDCEETPIEAALAEAETVPFFGERRVILIKHPYFFTSEKEKEIEHDLAK | 100 |
| LEAYLKAPSPFSIVVFFAPYEKLDERKKITKLAKESQEVVIAAPLAEEL | |
| RAWVRRRIESQGAQASDEAIDVLLRRAGTQLSALANEIDKLALFAGSGGT | 200 |
| IEAAAVERLVARTPEENVFVLVEQVAKRDI PAALQTFYDLLENNEEPIKI | |
| LALLAAHFRLLSQVKWLASLGYGQAQIAAALKVHPFRVKLALAQAARFAD | 300 |
| GELAEAINELADADYEVKSGAVDRRLAVELLMLRWGARPAQAGRHGR | |

FIG. 83

REPLACEMENT
SHEET

78/83

| | |
|---|-----|
| ATGCGATGGGAACAGCTAGCGAAACGCCAGCCGGTGGTGGCGAAAATGCT | |
| GCAAAGCGGCTTGGA AAAAGGGCGGATTTCTCATGCGTACTTGTTTGAGG | 100 |
| GGCAGCGGGGACGGGCAAAAAGCGGCCAGTTTGTTGTTGGCGAAACGT | |
| TTGTTTTGTCTGTCCCCAATCGGAGTTTCCCCGTGTCTAGAGTGCCGCAA | 200 |
| CTGCCGGCGCATCGACTCCGGCAACCACCCTGACGTCCGGGTGATCGGCC | |
| CAGATGGAGGATCAATCAAAAAGGAACAAATCGAATGGCTGCAGCAAGAG | 300 |
| TTCTCGAAAACAGCGGTTCGAGTCGGATAAAAAAATGTACATCGTTGAGCA | |
| CGCCGATCAAATGACGACAAGCGCTGCCAACAGCCTTCTGAAATTTTTTG | 400 |
| AAGAGCCGCATCCGGGGACGGTGGCGGTATTGCTGACTGAGCAATACCAC | |
| CGCCTGCTAGGGACGATCGTTTCCCGCTGTCAAGTGCTTTCGTTCCGGCC | 500 |
| GTTGCCCGCCGGCAGAGCTCGCCCAGGGACTTGTCGAGGAGCACGTGCCGT | |
| TGCCGTTGGCGCTGTTGGCTGCCCATTTGACAAACAGCTTCGAGGAAGCA | 600 |
| CTGGCGCTTGCCAAAGATAGTTGGTTTGCCGAGGCGCGAACATTAGTGCT | |
| ACAATGGTATGAGATGCTGGGCAAGCCGGAGCTGCAGCTTTTGTTTTTCA | 700 |
| TCCACGACCGCTTGTTTCCGCATTTTTTGGAAAGCCATCAGCTTGACCT | |
| GGACTTG | 757 |

FIG. 84

| | |
|---|-----|
| MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRGTKKAASLLLA KR | |
| LFCLSPIGVSPCLECRNCRRIDSGNHPDVRVIGPDGGSIKKEQIEWLQQE | 100 |
| FSKTAVESDKKMYIVEHADQMTTSAANSLLKFLEEPHPGTVAVLLTEQYH | |
| RLLG TIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA | 200 |
| LALAKDSWF AEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL | |
| GL | 252 |

FIG. 85

REPLACEMENT SHEET

79/83

| | |
|---|------|
| GTGGCATACCAAGCGTTATATCGCGTGTTTCGGCCGCAGCGCTTTGCGGA | |
| CATGGTCGGCCAAGAACACGTGACCAAGACGTTGCAAAGCGCCCTGCTTC | 100 |
| AACATAAAATATCGCACGCTTACTTATTTTCCGGCCCGCGCGGTACAGGA | |
| AAAACGAGCGCAGCGAAAATTTTCGCCAAGGCGGTCAACTGTGAACAGGC | 200 |
| GCCAGCGGCGGAGCCATGCAATGAGTGTCAGCTTGCCTCGGCATTACGA | |
| ATGGAACGGTTCCCGATGTGCTGGAAATTGACGCTGCTTCCAACAACCGC | 300 |
| GTCGATGAAATTTCGTGATATCCGTGAGAAGGTGAAATTTGCGCCAACGTC | |
| GGCCCGCTACAAAGTGTATATCATCGACGAGGTGCATATGCTGTGATCG | 400 |
| GTGCGTTTAACGCGCTGTTGAAAACGTTGGAGGAGCCGCCGAAACACGTC | |
| ATTTTCATTTTGGCCACGACCGAGCCGCACAAAATTCCGGCGACGATCAT | 500 |
| TTCCCGCTGCCAACGGTTCGATTTTCGCCGCATCCCGCTTCAGGCGATCG | |
| TTTCACGGCTAAAGTACGTGCAAGCGCCCAAGGTGTCGAGGCGTCAGAT | 600 |
| GAGGCATTGTCCGCCATCGCCCGTGCTGCAGACGGGGGGATGCGCGATGC | |
| GCTCAGCTTGCTTGATCAAGCCATTTTCGTTTCAGCGACGGGAACTTCGGC | 700 |
| TCGACGACGTGCTGGCGATGACCGGGGCTGCATCATTGCGCCCTTATCG | |
| AGCTTCATCGAAGCCATCCACCGCAAAGATACAGCGGCGGTTCTTCAGCA | 800 |
| CTTGGAACGATGATGGCGCAAGGGAAAGATCCGCATCGTTTGGTTGAAG | |
| ACTTGATTTTGTACTATCGCGATTTATTGCTGTACAAAACCGCTCCCTAT | 900 |
| GTGGAGGGAGCGATTCAAATTGCTGTCGTTGACGAAGCGTTCACTTCACT | |
| GTCGGAATGATTCCGGTTTCCAATTTATACGAGGCCATCGAGTTGCTGA | 1000 |
| ACAAAAGCCAGCAAGAGATGAAGTGGACAAACCACCCGCGCCTTCTGTTG | |
| GAAGTGGCGCTTGTGAAACTTTGCCATCCATCAGCCGCCGCCCGCTCGCT | 1100 |
| GTCGGCTTCCGAGTTGGAACCGTTGATAAAGCGGATTGAAACGCTGGAGG | |
| CGGAATTGCGGCGCCTGAAGGAACAACCGCCTGCCCTCCGTGACCGCC | 1200 |
| GCGCCGGTGAAAAAACTGTCCAAACCGATGAAAACGGGGGGATATAAAGC | |
| CCCGGTTGGCCGCATTTACGAGCTGTTGAAACAGGCGACGCATGAAGATT | 1300 |
| TAGCTTTGGTGAAAGGATGCTGGGCGGATGTGCTCGACACGTTGAAACGG | |
| CAGCATAAAGTGTGCGCACGCTGCCTTGCTGCAAGAGAGCGAGCCGTTGC | 1400 |
| AGCGAGCGCCTCAGCGTTTGTATTAAAATTCAAATACGAAATCCACTGCA | |
| AAATGGCGACCGATCCCACAAGTTCGGTCAAAGAAAACGTCGAAGCGATT | 1500 |
| TTGTTTGAGCTGACAAACCGCCGCTTTGAAATGGTAGCCATTCCGGAGGG | |
| AGAATGGGGAAAAATAAGAGAAGAGTTCATCCGCAATAAGGACGCCATGG | 1600 |
| TGGAAAAAAGCGAAGAAGATCCGTTAATCGCCGAAGCGAAGCGGCTGTTT | |
| GGCGAAGAGCTGATCGAAATTAAAGAA | 1677 |

FIG. 86

REPLACEMENT
SHEET

80/83

| | |
|---|-----|
| VAYQALYRVFRPQRFADMVGQEHVTKTLQSALLQHKISHAYLFSGPRGTG | |
| KTSAAKIFAKAVNCEQAPAAEPCNECPACLGITNGTVPDVLEIDAASNRR | 100 |
| VDEIRDIREKVKFAPTSARYKVYIIDEVHMLSIGAFNALLKTLEPPKHV | |
| IFILATTEPHKIPATIIISRCQRFDFRRIPLQAIVSRLKYVASAQGVEASD | 200 |
| EALSAIARAADGGMRDALSLDQAISFSDGKLRLDDVLAMTGAASFAALS | |
| SFIEAIHRKDTAAVLQHLETMMAQGKDPHRLVEDLILYYRDLLLYKTAPY | 300 |
| VEGAIQIAVVDEAFTSLSEMIPVSNLYEAIELLNKSQQEMKWTNHPRLLL | |
| EVALVKLCHPSAAAPSLSASELEPLIKRIETLEAELRRLKEQPPAPPSTA | 400 |
| APVKKLSKPMKTGGYKAPVGRIYELLKQATHEDLALVKGCWADVLDTLKR | |
| QHKVSHAALLQESEPVAASASAFVLKFKYEIHCKMATDPTSSVKENVEAI | 500 |
| LFELTNRRFEMVAIPEGEWGKIREEFIRNKDAMVEKSEEDPLIAEAKRLF | |
| GEELIEIKE | 559 |

FIG. 87

REPLACEMENT SHEET

81/83

| | |
|--|------|
| ATGGTGACAAAAGAGCAAAAAGAGCGGTTTCTCATCCTGCTTGAGCAGCT | |
| GAAGATGACGTCGGACGAATGGATGCCGATTTTCGTGAGGCAGCCATTC | 100 |
| GCAAAGTCGTGATCGATAAAGAGGAGAAAAGCTGGCATTTTTATTTTCAG | |
| TTCGACAACGTGCTGCCGGTTCATGTATACAAAACGTTTGCCGATCGGCT | 200 |
| GCAGACGGCGTTCCGCCATATCGCCGCCGTCCGCCATACGATGGAGGTCTG | |
| AAGCGCCGCGCGTAAGTGAAGGCGGATGTGCAGGCGTATTGGCCGCTTTGC | 300 |
| CTTGCCGAGCTGCAAGAAGGCATGTGCGCGCTTGTCGATTGGCTCAGCCG | |
| GCAGACGCCTGAGCTGAAAGGAAACAAGCTGCTTGTCGTTGCCCGCCATG | 400 |
| AAGCGGAAGCGCTGGCGATCAAACGGCGGTTGCCAAAAAAATCGCTGAT | |
| GTGTACGCTTCGTTTGCGTTTCCCCCCTTCAGCTTGACGTCAGCGTCGA | 500 |
| GCCGTCCAAGCAAGAAATGGAACAGTTTTTGGCGCAAAAACAGCAAGAGG | |
| ACGAAGAGCGAGCGCTTGCTGTACTGACCGATTTAGCGAGGGAAGAAGAA | 600 |
| AAGGCCGCGTCTGCGCCGCCGTCCGGTCCGCTTGTCATCGGCTATCCGAT | |
| CCGCGACGAGGAGCCGGTGCGGCGGCTTGAAACGATCGTCGAAGAAGAGC | 700 |
| GGCGCGTCGTTGTGCAAGGCTATGTATTTGACGCCGAAGTGAGCGAATTA | |
| AAAAGCGGCCGCACGCTGTTGACCATGAAAATCACAGATTACACGAACTC | 800 |
| GATTTTAGTCAAAATGTTCTCGCGCGACAAAGAGGACGCCGAGCTTATGA | |
| GCGGCGTCAAAAAGGCATGTGGGTGAAAGTGCGCGGCAGCGTGCAAAAC | 900 |
| GATACGTTTCGTCCGTGATTTGGTCATCATCGCCAACGATTTGAACGAAAT | |
| CGCCGCAACGAACGGCAAGATACGGCGCCGGAAGGGGAAAAGAGGGTCTG | 1000 |
| AGCTCCATTTGCATACCCCGATGAGCCAAATGGACGCGGTCACCTCGGTG | |
| ACAAAATCATTGAGCAAGCGAAAAAATGGGGGCATCCGGCGATCGCCGT | 1100 |
| CACCGACCATGCCGTTGTTTCAGTCGTTTCCGGAGGCCTACAGCGCGGCGA | |
| AAAAACACGGCATGAAGGTCATTTACGGCCTTGAGGCGAACATCGTCGAC | 1200 |
| GATGGCGTGCCGATCGCCTACAATGAGACGCACCGCCGTCTTTCGGAGGA | |
| AACGTACGTCGTCTTTGACGTCGAGACGACGGGCCTGTGCGGCTGTGTACA | 1300 |
| ATACGATCATTGAGCTGGCGGCGGTGAAAGTGAAAGACGGCGAGATCATC | |
| GACCGATTTCATGTCGTTTGCCAACCCTGGACATCCGTTGTGCGGTGACAAC | 1400 |
| GATGGAGCTGACTGGGATCACCGATGAGATGGTGAAAGACGCCCCGAAGC | |
| CGGACGAGGTGCTAGCCCGTTTTGTTGACTGGGCGGCGATGCGACGCTT | 1500 |
| GTTGCCACACGCCAGCTTTGACATCGGTTTTTTAAACGCGGGCCTCGC | |
| TCGCATGGGGCGCGGCAAAATCGCGAATCCAGTCATCGATACGCTCGAGC | 1600 |
| TGGCCCGTTTTTTTATACCCGGATTTGAAAAACCATCGGCTCAATACATTG | |
| TGCAAAAAATTTGACATTGAATTGACGCAGCATACCCGCGCCATCTACGA | 1700 |
| CGCGGAGGCGACCGGGCATTTGCTTATGCGGCTGTTGAAGGAAGCGGAAG | |
| AGCGCGGCATACTGTTTCATGACGAATTAAACAGCCGCACGCACAGCGAA | 1800 |
| GCGTCCATATCGGCTTGCGCGCCCGTTCATGTGACGCTGTTGGCGCAAAA | |
| CGAGACTGGATTGAAAAATTTGTTCAAGCTTGTCGTCATTGTCGCACATTC | 1900 |
| AATATTTTCACCGTGTGCCGCGCATCCCGCGCTCCGTGCTCGTCAAGCAC | |
| CGCGACGGCCTGCTTGTCGGCTCGGGCTGCGACAAAGGAGAGCTGTTTGA | 2000 |
| CAACTTGATCCAAAAGGCGCCGGAAGAAGTCGAAGACATCGCCCGTTTTTT | |
| ACGATTTTCTTGAAGTGATCCGCCGACGTGTACAAGCCGCTCATCGAG | 2100 |
| ATGGATTATGTGAAAGACGAAGAGATGATCAAAAACATCATCCGCAGCAT | |
| CGTCGCCCTTGGTGAGAAGCTTGACATCCCGGTTGTCGCCACTGGCAACG | 2200 |

FIG. 88A

REPLACEMENT SHEET

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| | |
|---|------|
| TCCATTACTTGAACCCAGAAGATAAAAATTTACCGGAAAATCTTAATCCAT | |
| TCGCAAGGCGGGGCGAATCCGCTCAACCGCCATGAACTGCCGGATGTATA | 2300 |
| TTTCCGTACGACGAATGAAATGCTTGACTGCTTCTCGTTTTTAGGGCCGG | |
| AAAAAGCGAAGGAAATCGTCGTTGACAACACGCAAAAAATCGCTTCGTTA | 2400 |
| ATCGGCGATGTCAAGCCGATCAAAGATGAGCTGTATACGCCGCGCATTGA | |
| AGGGGCGGACGAGGAAATCAGGGAAATGAGCTACCGGCGGGCGAAGGAAA | 2500 |
| TTTACGGCGACCCGTTGCCGAACTTGTTGAAGAGCGGCTTGAGAAGGAG | |
| CTAAAAAGCATCATCGGCCATGGCTTTGCCGTCATTTATTTGATCTCGCA | 2600 |
| CAAGCTTGTGAAAAAATCGCTCGATGACGGCTACCTTGTCGGGTCGCGCG | |
| GATCGGTCGGCTCGTCGTTTGTCGCGACGATGACGGAAATCACCGAGGTC | 2700 |
| AATCCGCTGCCGCCGCATTACGTTTGCCCGAACTGCAAGCATTTCGGAGTT | |
| CTTTAACGACGGTTCAGTCGGCTCAGGGTTTGATTTGCCGGATAAAAACT | 2800 |
| GCCCCGCGATGTGGGACGAAATACAAGAAAGACGGGCACGACATCCCGTTT | |
| GAGACGTTTCTCGGCTTTAAAGGCGACAAAGTGCCGGATATCGACTTGAA | 2900 |
| CTTTTCCGGCGAATACCAGCCGCGCGCCACAACATAACGAAAGTGCTGT | |
| TTGGCGAAGACAACGTCTACCGCGCCGGGACGATTGGCACGGTCGCTGAC | 3000 |
| AAAACGGCGTACGGATTTGTCAAAGCGTATGCGAGCGACCATAACTTAGA | |
| GCTGCGCGGCGCGGAAATCGACGGCTCGCGGCTGGCTGCACCGGGGTGAA | 3100 |
| GCGGACGACCGGGCAGCATCCGGGCGGCATCATCGTCGTCCCGGATTATA | |
| TGGAAATTTACGATTTTACGCCGATTCAATATCCGGCCGATGACACGTCC | 3200 |
| TCTGAATGGCGGACGACCCATTTGACTTCCATTCGATCCACGACAATTT | |
| GTTGAAGCTCGATATTCTCGGGCACGACGATCCGACGGTCATTCGCATGC | 3300 |
| TGCAAGATTTAAGCGGCATCGATCCGAAAACGATCCCGACCGACGACCCG | |
| GATGTGATGGGCATTTTCAGCAGCACCGAGCCGCTTGCGGTTACGCCGGA | 3400 |
| GCAAATCATGTGCAATGTCGGCACGATCGGCATTCCGGAGTTTGGCACGC | |
| GCTTCGTTTCGGCAAATGTTGGAAGAGACAAGGCCAAAAACGTTTTCCGAA | 3500 |
| CTCGTGCAAATTTCCGGCTTGTCGCACGGCACCGATGTGTGGCTCGGCAA | |
| CGCGCAAGAGCTCATTCAAACGGCACGTGTACGTTATCGGAAGTCATCG | 3600 |
| GCTGCCGCGACGACATTATGGTCTATTTGATTTACCGCGGGCTCGAGCCG | |
| TCGCTCGCTTTTAAAATCATGGAATCCGTGCGCAAAGGAAAAGGCTTAAC | 3700 |
| GCCGGAGTTTGAAGCAGAAATGCGCAAACATGACGTGCCGGAGTGGTACA | |
| TCGATTTCATGCAAAAAAATCAAGTACATGTTCCCGAAAGCGCACGCCGCC | 3800 |
| GCCTACGTGTTAATGGCGGTGCGCATCGCCTACTTTAAGGTGCACCATCC | |
| GCTTTTGTATTACGCGTCGTACTTTACGGTGCGGGCGGAGGACTTTGACC | 3900 |
| TTGACGCCATGATCAAAGGATCACCCGCCATTTCGCAAGCGGATTGAGGAA | |
| ATCAACGCCAAAGGCATTCAGGCGACGGCGAAAGAAAAAAGCTTGCTCAC | 4000 |
| GGTTCTTGAGGTGGCCTTAGAGATGTGCGAGCGCGGCTTTTCCTTTAAA | |
| ATATCGATTTGTACCGCTCGCAGGCGACGGAATTTCGTCATTGACGGCAAT | 4100 |
| TCTCTCATTTCCGCCGTTCAACGCCATTCCGGGGCTTGGGACGAACGTGGC | |
| GCAGGCGATCGTGCGCGCCCGCGAGGAAGGCGAGTTTTTGTGCAAGGAGG | 4200 |
| ATTTGCAACAGCGCGGCAAATTGTGCAAAACGCTGCTCGAGTATCTAGAA | |
| AGCCGCGGCTGCCTTGACTCGCTTCCAGACCATAACCAGCTGTCGCTGTT | 4300 |

T

FIG. 88B

REPLACEMENT SHEET

83/83

| | |
|---|------|
| MVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHIFYFQ | |
| FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLC | 100 |
| LAELQEGMSPLVDWLSRQTPPELKGKLLVVARHEAEALAIKRRFAKKIAD | |
| VYASFGFPPLQLDVSVEPSKQEMEQLAQKQEQEDEERALAVLTDLAREEE | 200 |
| KAASAPPSGPLVIGYPIRDEEPVRRLETIVEEERRVVVQGYVFD AEVSEL | |
| KSGRTLTLTKITDYTNSILVKMFSRDKEDAEELMSGVKKGMWVKVRGSVQN | 300 |
| DTFVRDLV I IANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV | |
| TKLIEQAKKWGHPAIAVTDHAVVQSFPEAYSAAKKHGMKVIYGLEANIVD | 400 |
| DGVPIAYNETHRRLSEETYVVFDVETTGLSAVYNTI IELAAVKVKDGEI I | |
| DRFMSFANPGHPLSVTTMELTGITDEMVKDAPKPDEVLARFVDWAGDATL | 500 |
| VAHNASFDIGFLNAGLARMGRGKIANPVIDTLELARFLYPDLKNHRLNTL | |
| CKKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFHDDELNSRTHSE | 600 |
| ASYRLARPFHVTLTLLAQNETGLKNLFLKLVSLSHIQYFHRVPRIPRSVLVKH | |
| RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIE | 700 |
| MDYVKDEEMIKNI IRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIH | |
| SQGGANPLNRHEL PDVYFRTTNEMLD CFSFLGPEKAKEI VVDNTQKIASL | 800 |
| IGDVKPIKDELYTPRIEGADEEIREMSYRRAKEIYGDPLPKLVEERLEKE | |
| LKSIIGHGFAVIYLI SHKLVKKSLDDGYLVGSRGSGVSSFVATMTEITEV | 900 |
| NPLPPHYVCPNCKHSEFFNDGSGVSGFDLPDKNCPRCGTTYKKDGHDI PF | |
| ETFLGFKGDKVPDIDLNFSGEYQPRAHNYTKVLFGEDNVYRAGTIGTVAD | 1000 |
| KTAYGFVKAYASDHNLELRGAEIDLAAGCTGVKRTTGQHPGGIIVVPDYM | |
| EIYDFTPIQYPADDTSSSEWRTHFDFHSHIDNLLKLDILGHDDPTVIRML | 1100 |
| QDLSGIDPKTIPTDDPDVMGIFSSTEPLGVTPEQIMCNVGTIGIPEFGTR | |
| FVRQMLEETRPKTFSELVQISGLSHGTDVWLGN AQELIQNGTCTLSEVIG | 1200 |
| CRDDIMVYLIYRGLEPSLAFKIMESVRKGKGLTPEFEAEMRKHDVPEWYI | |
| DSCCKIKYMFPAHAAAYVLM AVRIAYFKVHHPLLYASYFTVRAEDFDL | 1300 |
| DAMIKGSPAIRKRIEEINAKGIQATAKEKSLTVLEVALEM CERGF S FKN | |
| IDLYRSQATEFVIDGNSLI PPFNAIPGLGTNVAQAIVRAREEGEFLSKED | 1400 |
| LQQRGKLSKTLLEYLESRGCLDSLPHNQLSLF | |

FIG. 89